

GenCore version 5.1.4-p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - protein search, using frame_plus_nzp model

Run on: May 7, 2003, 15:25:19 ; Search time 92 Seconds
(without alignments)

Title: US-09-965-830-1_COPY_6_3257
Perfect score: 6089
Sequence: 1 atgcgcgcacatgcggggcct.....aagaagcagcaggggtctga 3252

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Delop 6.0 , Delext 7.0

Searched: 349150 seqs, 92025710 residues

Total number of hits satisfying chosen parameters: 698300

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+nzp.model -DEV=xlp
-O=/cgn2_1/USPROOOL/US09965830/runat_07052003_151452_6401/app.query.fasta_1.3399
-DB=Published_Applications_AA -OFMT=faстан -SUFFIX=rapb -MINMATCH=0.1
-IOOCTL=0 -IOOEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US09965830.ecgn_1_1_37_@runat_07052003_151452_6401
-NCPU=6 -ICPU=3 -NO_XLPTX -NO_MAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FCAPOP=6
-FCAPEXT=7 -YGAPOP=10 -YCAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published_Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCU_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5704	93.7	1083	9	US-09-965-830-2
2	5698	93.6	1083	9	US-10-160-224-1
3	5659	92.9	1080	10	US-09-119-855-2
4	5649.5	92.8	1082	9	US-10-121-746-20

5	2461.5	40.4	1017	9	US-09-965-830-6
6	1901	31.2	1284	9	US-10-160-224-9
7	1801	31.2	1284	10	US-09-119-855-11
8	1835.5	30.1	542	10	US-09-119-855-5
9	1551	25.5	1159	9	US-10-000-151B-3
10	1551	25.5	1159	9	US-10-193-692-5
11	1551	25.5	1159	10	US-09-735-995-2
12	1551	25.5	1159	10	US-09-735-995-4
13	1551	25.5	1159	10	US-09-735-995-2
14	1509.5	24.8	994	10	US-09-119-855-10
15	1487	24.4	290	10	US-09-119-855-8
16	1486.5	24.4	958	9	US-10-192-440-2
17	1475	24.2	950	9	US-10-192-440-9
18	1432	23.5	1177	9	US-10-192-440-9
19	1405.5	23.1	1186	9	US-10-193-692-4
20	1395.5	22.9	1195	9	US-10-193-692-2
21	1378.5	22.6	962	9	US-10-188-308-24
22	1378	22.6	960	9	US-10-188-308-21
23	1370.5	22.5	989	9	US-10-188-308-23
24	1369	22.5	962	9	US-10-188-308-3
25	1367.5	22.5	987	9	US-10-188-308-22
26	1358.5	22.3	989	9	US-10-188-308-4
27	1339.5	22.0	988	9	US-09-875-321-12
28	1339.5	22.0	988	9	US-10-162-012-12
29	1332.5	21.9	988	9	US-09-875-321-5
30	1332.5	21.9	988	9	US-10-162-012-5
31	1331	21.9	988	9	US-10-128-323-2
32	566	9.3	1203	9	US-10-067-457-3
33	536	8.8	521	10	US-09-813-320-4
34	532	8.7	889	9	US-10-067-457-1
35	531	8.7	875	9	US-09-548-933-15
36	530	8.7	530	10	US-09-813-320-2
37	513	8.4	863	9	US-10-067-457-5
38	484	7.9	890	9	US-10-158-684-4
39	484	7.9	890	9	US-10-158-684-4
40	475.5	7.8	774	9	US-10-158-711-1
41	475.5	7.8	774	9	US-10-158-684-10
42	475.5	7.8	774	9	US-10-158-711-10
43	449.5	7.4	749	9	US-09-548-933-1
44	429.5	7.1	254	9	US-09-548-933-16
45	424.5	7.0	694	9	US-09-842-758-75

ALIGNMENTS

RESULT 1
US-09-965-830-2
; Sequence 2, Application US/09965830
; Patent No. US20020177201A1
GENERAL INFORMATION:
; APPLICANT: Yamamouchi Pharmaceutical Co., Ltd.
; TITLE OF INVENTION: A novel potassium channel protein
; FILE REFERENCE: Y9903-PCT
CURRENT APPLICATION NUMBER: US/09/965, 830
PRIOR APPLICATION NUMBER: 2001-10-01
PRIOR FILING DATE: 2001-07-21
PRIOR APPLICATION NUMBER: JP P1998-346198
PRIOR FILING DATE: 1998-12-04
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 1083
TYPE: PRT
ORGANISM: Homo sapiens
US-09-965-830-2

Alignment Scores:
Pred. No.: 3.65e-275
Score: 5704.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 93.68%
Length: 1083
Matches: 1083
Conservative: 0
Mismatch: 0
Indels: 0

161 LysGlyPheAsnAlaAsnArgArgSerArgAlaValLeuTyrHisLeuSerGlyHis 180
541 CTGCAAGACACCCCAAGGCAAGCAAGCTCAATAGGGGGTGTGGGAGAAACA 600
181 LeuGlnLysGlnProLysGlyLysHisLysLeuAsnLysGlyValPheGlyGlnLysPro 200
601 AACTGGCCCTGATACAAATAGCCGCCGCAAGTCCGACCCCTTCATCCCTGTGCACTG 660
201 AsnLeuProGlnTyrLysValAlaAlaIleArgLysSerProPheIleLeuLeuHisLys 220
661 GGGGCACTGAGAGCCACCTGGATGGCTTCATCCCTGCTGCCACACTATATGGCTGTC 720
221 GlyAlaLeuArgAlaThrThrPheSerGlyPheIleLeuLeuAlaThrLeuTyrValAlaVal 240
721 ACGTGGCCCTACAGCTGTGTGTGTGACACAGCAAGGAGGCCAGTGGCCGCCGCCGCCG 780
241 ThrValProTyrSerValLysValSerThrAlaArgGlnProSerAlaAlaArgGlyPro 260
781 CCCAGGCTGTGACCTGGCCGTGGAGGCTCTTCATCTCTGACATGTGCTGAATTC 840
261 ProSerValLysAsnLeuAlaValGlnValLeuPheIleLeuAsnProIleValLeuAsnPro 280
841 CGTACACATTCGTGTCCAACTGAGTGGGGGAGTGGTGTGGCCCAAGTCCATTTGCTC 900
281 ArgThrThrPheValSerLysSerGlyGlnValAlaPheAlaProLysSerIleCysLeu 300
901 CACTACCTACCACTGGTTCCTGCTGATGTCAATCCAGAGCTGCCCTTACCTGCTA 960
301 HisTyrValThrThrThrPheLeuLeuAsnProIleAlaAlaLeuProPheAsnLeu 320
961 CATGCTTCATAGTTCATACCTGACTTGGGGCCCAATCTGCTGAGAGGCTGGCTGCTG 1020
321 HisAlaPheLysValAlaValLysTyrPheGlyAlaHisLeuLysTyrValArgLeuLeu 340
1021 CGCCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080
341 ArgLeuLeuArgLeuLeuProArgLeuAsnProArgLysSerGlnTyrSerAlaValLeu 360
1081 ACCTGCTCAGTGGCCGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
361 ThrLeuLeuMetAlaValPheAlaLeuLeuAlaHisTyrValAlaCysValThrPheTyr 380
1141 AATGGCCAGCGGAGATGAGAGCAAGCAATCCGAGCTGCTGAGATGGCTGCTGCTGCTG 1200
381 IleGlyGlnArgGlnIleGlnSerSerGlnSerGlnLeuProGlnIleGlyLysLeuGln 400
1201 GAGCTGGCCCGCGAGTGAAGTCCCTACCTACCTGCTGCTGCTGCTGCTGCTGCTGCTG 1260
401 GlnLeuAlaArgArgLeuLysProTyrTyrLeuValGlyArgProAlaGlyGly 420
1261 AACAGCTCCGCGCAGAGTACAACTGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1320
421 AsnSerSerGlyLysSerAsnSerSerSerSerSerSerSerSerSerSerSerSerSer 440
1321 GAGCTGCTGGGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380
441 GlnLeuLeuGlyGlyProSerLeuArgSerAlaTyrIlePheSerLeuTyrPheAlaLeu 460
1381 AGCAGCTCAGCAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440
461 SerSerLeuThrSerValGlyPheGlyAsnValSerAlaAsnThrSerPheGlnLysIle 480
1441 TTCTCATCTGACACATGCTCATGCGCGCTGATGCAAGCGGCTGCTGCTGCTGCTGCTGCT 1500
481 PheSerIleCysThrMetLeuIleGlyAlaLeuMetHisAlaValPheGlyAsnVal 500
1501 ACGGCAATTCACGCGCATGTACGCGCGCGCTTCTGTACACAGCAGCAGCAGCAGCAGCAG 1560
501 ThrAlaIleIleGlnArgMetTyrAlaArgArgPheLeuTyrHisSerArgThrArgAsp 520
1561 CTGGCGCAGTACATCCGATCCACCGTATCCCAAGCCCTCAAGCAGCGGCTGCTGAG 1620

521 LeuArgAspTyrIleArgIleHisArgIleProLysProLeuLysGlnArgMetLeuGln 540
1621 TACTTCCAGGCCACCGGGCGGAGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCA 1680
541 TyrPheGlnAlaThrThrPheAlaValAsnAsnGlyIleAspThrThrGlnLeuLeuGlnSer 560
1681 CTCCCTGACAGCTGCGCGCAGACATGCGCATGCACTGCAAGAGAGTCTGCAAGCTG 1740
561 LeuProAspGlnLeuArgAlaAspIleAlaMetHisLeuHisLysGlnValLeuGlnLeu 580
1741 CCAGCTTTGAGCGGCGCAGCAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1800
581 ProLeuPheGlnAlaAlaSerArgLysCysLeuArgAlaLeuSerLeuAlaLeuArgPro 600
1801 GCGTGTGACAGCGCGCGCGAGTACATCCATCCAGGCGGATGCGCGCGCGCGCGCTTAC 1860
601 AlaPheCysThrProGlyGlnTyrLeuIleHisGlnIleLysPheAlaLeuGlnAlaLeuTyr 620
1861 TTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1920
621 PheValLysSerGlySerMetGlnValLeuLysGlyLysThrValLeuAlaIleLeuGly 640
1921 AAGGCGCAGCTGATCGGCTGTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1980
641 LysGlnLysPheLysIleGlyCysGlnLeuProArgArgGlnValValLysAlaAsnAla 660
1981 GACGTGAAGGGCTGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2040
661 AspAlaLysGlyLeuThrTyrCysValLeuGlnCysLeuGlnLeuAlaGlyLeuHisAsp 680
2041 AGCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2100
681 SerLeuAlaLeuTyrProGlnPheAlaProArgPheSerArgGlyLeuArgGlyLeuLeu 700
2101 AGCTCAACCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2160
701 SerTyrAsnLeuGlyAlaGlyGlySerAlaGlnValAspPheSerSerLeuSerGly 720
2161 GACCAATACCTTATGCTCAAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2220
721 AsnAsnThrLeuMetSerThrLeuGlnGlnLysGlnThrAspGlyGlnIleLysProThr 740
2221 GTTCCCGCCAGCCAGCTGATGAGCCCTCAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTG 2280
741 ValSerProAlaProAlaAspGlnProSerSerProLeuLeuSerProLysTyrThrSer 760
2281 TCAATCTCAGCTGCAAGCTGCTATCCCAAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCT 2340
761 SerSerSerAlaAlaLysLeuLeuSerProArgArgThrAlaProArgProArgLeuGly 780
2341 GGCAGAGGAGCGCAGGCGAGGCGGCTTGAAGCTGAGAGCTGAGCTGAGCTGAGCTGCTG 2400
781 GlyArgGlyArgProGlyArgAlaGlyAlaLeuLysAlaGlnAlaGlyProSerAlaPro 800
2401 CCACGGGCGCTTACAGGCGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2460
801 ProArgAlaLeuGlnIleGlyLeuArgLeuProPheProPheProPheProPheProPhe 820
2461 AGCCCGCAGCTAGTACATGAGTGAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2520
821 SerProArgValAlaAspGlyIleGlnAspGlyCysGlySerAspGlnProLysPheSer 840
2521 TTCCGCGTGGCGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2580
841 PheArgValGlyGlnSerGlyProGlnCysSerSerSerSerSerSerSerSerSerSer 2640
2641 GGCCTGCTCACTGTTCCCAATGGCGCGCAGGAGGCAAGCAACAGCACTGAGACAG 2640
861 GlyLeuLeuThrValProHisGlyProSerGlnAlaArgAsnThrAspThrLeuAspLys 880
2641 CTGGCGCAGGCGGAGAGAGAGCTGCAAGAGAGAGTGTGAGATGCGGAGAGAGAGTGCAG 2700
881 LeuArgGlnAlaValThrGlnLeuSerGlnIleValLeuGlnMetArgGlnGlyLeuGln 900

QY 2701 TCACCTTCAGGCTGTGACAGCTTGTCTGGCGCCACAGAGGAGGCTCCGCTCCG 2760
 Db 901 SerLeuArgGlnAlaValGlnLeuValLeuAlaProHisArgGlnGlyProCysProArg 920
 QY 2761 GCATCGGGAGAGGGCGCTGCCAGCCAGCAGCTCCGGGGTTGTGACGCTGTGTGTG 2820
 Db 921 AlaSerGlyGlnGlyProCysProAlaSerThrSerGlyLeuLeuGlnProLeuGlyVal 940
 QY 2821 GACACTGGGGGATCTCTCTACTGCTGACAGCCCGCAGCTGCTCTGTCTGATGGAGCT 2880
 Db 941 AspThrGlyAlaSerSerThrCysLeuGlnProAlaGlySerValLeuSerGlyThr 960
 QY 2881 TGGCCCCACCTCGTCCGGGGCTCTCCCTCATGGACCCCTGGCCCTGGGGTCCCGCA 2940
 Db 961 TrpProHisProAlaProGlyProProProLeuMetAlaProTrpProTrpGlyProPro 980
 QY 2941 GCGTCTCAGAGCTCCCGCTGGGCTCGAGCCAGCAGCTTGTGACCTTCACCTCAGACTCA 3000
 Db 981 AlaSerGlnSerSerProTrpProArgAlaThrAlaPheTrpThrSerThrSerAspSer 1000
 QY 3001 GAGCCCCCTGCTCAGAGAGCTGTCTGTGAGCCAGCAGCCCTGCTCCCTCTCTCT 3060
 Db 1001 GluProProAlaSerGlyAspLeuGlySerGluProSerThrProAlaSerProProPro 1020
 QY 3061 TCTGAGGAAGGGGCTAGAGACTGGCCCGCAGAGCTGTGAGCCAGGCTAGGCTACAGAC 3120
 Db 1021 SerGlnGlnGlyAlaArgThrGlyProAlaGluProValSerGlnAlaGlnAlaThrSer 1040
 QY 3121 ACTGAGAGCCCGCCAGCAGAGGCTCAGGGGGCTGGCTGGCCCTGGAGCCCGCCAGAGCTG 3180
 Db 1041 ThrGlyGluProProProGlySerGlyGlyLeuAlaLeuProTrpAspProHisSerLeu 1060
 QY 3181 GAGATGGGCTTATGGTGCAGTGGCTGTGACAGCTGTGACAGCTCAGTCCAGGAGAGG 3240
 Db 1061 GlnMetValLeuLeuGlyCysHisGlySerGlyThrValGlnTrpThrGlnGlnGlnGly 1080
 QY 3241 ACAGGGGCTC 3249
 Db 1081 ThrGlyVal 1083

RESULT 3
 US-09-119-855-2
 ; Sequence 2, Application US/09119855
 ; Patent No. US2002009197A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Curtis, Roy A.J.
 ; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
 ; FILE REFERENCE: mmi-055
 ; CURRENT APPLICATION NUMBER: US/09/119,855
 ; CURRENT FILING DATE: 1998-07-21
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 2
 ; LENGTH: 1080
 ; TYPE: PRT
 ; ORGANISM: Monkey
 ; US-09-119-855-2
 Alignment Scores:
 Pred. No.: 6,19e-273 Length: 1080
 Score: 5659.00 Matches: 1075
 Percent Similarity: 99.63% Conservative: 1
 Best Local Similarity: 99.54% Mismatches: 4
 Query Match: 92.94% Indels: 0
 DB: 10 Gaps: 0
 US-09-965-830-1_COPY_6_3257 (1-3252) x US-09-119-855-2 (1-1080)
 QY 10 ATGCGGGGCTCTGCGGCTCGAGACACTTCTGACACCATCGCTACGCGCTTCGAC 69
 Db 1 MetArgGlyLeuLeuAlaProGlnAsnThrPheLeuAspThrIleAlaThrArgPheAsp 20

QY 70 GGCACGACAGTAATCTGTCGTGGGCAAGCCAGGAGGGGGCTTCCCGGTGTC 129
 Db 21 GlyThrHisSerAsnPheValLeuGlyAsnAlaGlnAlaGlyLeuPheProValVal 40
 QY 130 TACTGCTCTATGGCTTCTGTGTGACCTCAGCGGCTTCTCCGGGCTGAGTCAATCAGCGG 189
 Db 41 TyrCysSerAspGlyPheCysAspLeuThrGlyPheSerArgAlaGlyValMetGlnArg 60
 QY 190 GCGTGTCCCTGCTCTCTTATGGGCAACACAGTACAGCTCTCCGCAACAGATC 249
 Db 61 GlyCysAlaCysSerPheLeuThrGlyProAspThrSerGluLeuValArgGlnGlnIle 80
 QY 250 CGCAGGCGCTTGACGACGACGACGAGCTTAAGCTGAGCTGATCTGTACCGGAGAGC 309
 Db 81 ArgValAlaLeuAspGlnHisGlyGluPheGlyAlaGlyIleLeuValLeuValArgGlySer 100
 QY 310 GGGCTCCGCTTGTGTCCTCGATGATGCCATTAAGAATGAAAGGAGAGTG 369
 Db 101 GlyLeuProPheTrpPheCysLeuLeuAspValIleProIleCysAsnArgGlyGlyVal 120
 QY 370 GCTCTCTCTACTCTCTCACAAGACATCAGCGAACAACGAGAGGGGGCGCCGAC 429
 Db 121 AlaLeuPheLeuValSerHisLysAspIleSerGlnThrLysAsnArgGlyGlyProAsp 140
 QY 430 AGATGAGAGAGACAGAGTGGTGGCGCGCCGATATGCGCGGACAGATCAAGAGCTTC 489
 Db 141 ArgTrpLysGlyThrGlySerGlyArgArgArgGlyGlyArgAlaArgSerLysGlyPhe 160
 QY 490 AATGCCAACCGGCGGGGAGCGGGCGCTGTACCACTGTCCGGGACCTGCAAGAG 549
 Db 161 AsnAlaAsnArgArgArgSerArgAlaValLeuValHisLeuSerGlyHisLeuGlnLys 180
 QY 550 CAGCCCAAGGGGACAGACAGTCAATAGGGGGCTTGGGAGAACCAACTGCT 609
 Db 181 GlnProLysGlyLysHisLysLeuAsnLysGlyValPheGlyGlyLysProAsnLeuPro 200
 QY 610 GAGTACAAAGTAGCCGCCATCCGGAAGTGCCTTCATCCTGTGACAGTGGGGGACAG 669
 Db 201 GluTyrLysValAlaAlaIleArgLysSerProPheIleLeuLeuHisCysGlyAlaLeu 220
 QY 670 AGAGCCAGCTGGAGTGGCTTCATCTGCTCGCACACTATGTGGCTGCTACCTGGCCC 729
 Db 221 ArgAlaThrTrpAspGlyPheIleLeuLeuAlaThrIleValAlaValThrValPro 240
 QY 730 TACACGCTGTGTGACAGACAGCAGGAGGCCAGCTGCCCGCGCGCCGCGCAGCGTC 789
 Db 241 TyrSerValCysValSerThrAlaArgGluProSerAlaAlaArgGlyProProSerVal 260
 QY 790 TGTGACCTGGCGGTGAGGCTCTCTTCACTTGCATTTGCTGTAATTCGATCCAGACA 849
 Db 261 CysAspLeuAlaValGlnValLeuPheIleLeuAspIleValLeuAsnPheArgThr 280
 QY 850 TTCGTGTCAGTGGGCGGCGAGTGGTGTGGCCCAAGTGCATTTGCTGCTCAGTACGTC 909
 Db 281 PheValSerLysSerGlyGlnValValPheAlaProLysSerIleCysLeuHisGlyVal 300
 QY 910 ACCACTGTGCTCTGTGATGTCATCGCAGCGCTGCTTGAACCTGCTCAATGCGCTTC 969
 Db 301 ThrThrTrpPheLeuLeuAspValIleAlaAlaLeuProPheAspLeuHisAlaPhe 320
 QY 970 AAGGTCAACGTGTACTTCGGGGCCCATCTGCTGAAGAGTGGCGCTGCTGCTGCTGCTG 1029
 Db 321 LysValAsnValTyrPheGlyAlaHisLeuLeuLysThrValArgLeuLeuArgLeuLeu 340
 QY 1030 CGCGTCTCGCGGCGGTGAGCCGCTACTCGCAGTACAGCGCGCTGTGCTGACACTGTC 1089
 Db 341 ArgLeuLeuProAlaGlyLeuAspArgTyrSerGlnTyrSerAlaValIleLeuThrLeuLeu 360
 QY 1090 ATGCGCGTGTTCGCGCTGCTGCGCACTGGGTGCGCTGCGCTGCTTACATTGGCCAG 1149
 Db 361 MetAlaValPheAlaLeuLeuAlaHisTrpValAlaCysValTrpPheTyrIleGlyGln 380
 QY 1150 CGGAGATCGAGAGCAGCAGATCCGAGCTGCTGAGATGGCTGGCTGCGAGAGCTGGCC 1209


```

1  APPLICANT: Hu, Ping
2  APPLICANT: Rutter, Marc
3  APPLICANT: Wang, Jian-Wang
4  TITLE OF INVENTION: No. US20030036648a1el Human Potassium Channels
5  FILE REFERENCE: SEQ-15P
6  CURRENT APPLICATION NUMBER: US/10/121,746
7  CURRENT FILING DATE: 2002-04-11
8  PRIOR APPLICATION NUMBER: US/09/336,643A
9  PRIOR FILING DATE: 1999-06-18
10 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/076,687
11 PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-07
12 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/116,448
13 PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-19
14 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US99/03826
15 PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-22
16 NUMBER OF SEQ ID NOS: 87
17 SOFTWARE: FASTSEQ for Windows Version 4.0
18 SEQ ID NO 20
19 LENGTH: 1082
20 TYPE: PRT
21 ORGANISM: H. sapiens
22 US-10-121-746-20

```

```

Alignment Scores:
Pred. No.:      1,836,272      Length:      1082
Score:          5649.50        Matches:      1076
Percent Similarity: 99.35%    Conservative: 0
Best Local Similarity: 99.35%  Mismatches:  6
Query Match:    92.76%        Indels:      1
DB:             9             Gaps:        1

US-09-965-830-1_COPY_6_3257 (1-3252) x US-10-121-746-20 (1-1082)

```

OY	1	AGCGGGCCATGGGGGGCCCTCGTGGCGCCTCAGAACACCTCTCCGAGCAACATCGCTAGC	60
Db	1	MeCPtoLaMeLtrgLyLeuLeuAlaProGlnAsnThrPheLeuAspThrIleAlaThr	20
OY	61	CGCTTGACGGCGACGGACAGTACTCTCGTGGCGGACGCCAGGTGGGGGCTCTTC	12
Db	21	ArgPheAspLeuThrHisSerAsnPheValLeuGlyAsnAlaSer---GlyGlyAlaLeu	39
OY	121	CCCGTGGCTACGCTCTCATATGGCTCTGTGACCTCAGCGGCTTCCCGGGCTAGGTC	18
Db	40	ProValValIYrCYSerSerAspLeuPheCYAspLeuThrGlyPheSerArgLaGluVal	59
OY	181	ATGCACGGGGGCTGTGCTCTCTCTCTTATGGCGGAGACAGAGTAGCTGTCTCCG	24
Db	60	MetGlnArgGlyCYsAlaCYSerPheLeuIYrGlyProAspThrSerGluLeuValArg	79
OY	241	CAACAGATCCGAAAGGCCCTGGACAGACACAAGAGATTCAAGCGTAGCTGATCTCTAC	30
Db	80	GlnGlnIleArgLyAlaLeuAsnArgLinhIstLysGluPheIYrAlaGluLeuIleLeuIYr	99
OY	301	CGAAGAGCGGGCTCCCTCTCTGCTGTCTCTGATGTGATACCATTAAGATGAGAAA	360
Db	100	ArgLysSerGlyLeuProPheTrpLysLeuAsnValIleProIleLysAsnGluLys	119
OY	361	GGGAGGTGGGCTCTTCTAGTCTCTCAACAGACATCAGCGAAACCAACAGACCGAGG	420
Db	120	GlyGluValAlaLeuPheLeuValSerHisLysAspLieserGluThrLysAsnArgGly	139
OY	421	GGCCCCGACAGATGGAAAGAGACAGAGTGGTGGCGGGCGCGCATATGGCGGGACAGATCC	480
Db	140	GlyProAspArgTrpLysGluThrPheIYrGlyLeuArgArgIYrGlyArgAlaArgSer	159
OY	481	AAAGGCTTCAATGCCAACCGCGGGCGGAGCGGGCGCGGTCTACACCTGTCCGGGCAC	540
Db	160	LysGlyPheAsnAlaAsnArgArgSerArgAlaValLeuIYrHisLeuSerGlyHis	179
OY	541	CTGCAGAAAGACGCCCCAAGGCGACACACAAGTCAATAGAGGGGTGTGGGGAGAAACA	600
Db	180	LeuGlnLysGlnProLysGlyLysHisLysLeuAsnLysGlyAlaPheGlyGlyLysPro	199

QY	601	AACTGCTCTAGTACAAAGTAGCCGCATCCGGAGTCCGGCTTCACTCCGTGGCACTGT	660
Db	200	AsnLeuProGlnTyrLysValAlaAlaIleArgLysSerProhelleuLeuHsLysCys	219
QY	661	GGGGCACTGAGACCACACCTGGGATGGCTTCATCCTCTGCGCCACACTCATGAGCTGC	720
Db	220	GlyAlaLeuArgAlaThrTrpAspGlyPheIleLeuLeuAlaThrLeuTyrAlaAlaVal	239
QY	721	ACTGTACCCGTACAGCGGTGTGTGTGAGACACAGCAGCGGAGCCAGTCCGCCCGCGCCG	780
Db	240	ThrValProTyrSerValLysValSerThrAlaArgGlnProSerAlaAlaArgGlyPro	259
QY	781	CCGAGCGTGTGACCTGGCCGCGGAGGCGTCCTTCATCCCTTGACATTGTGCTGAATTC	840
Db	260	ProSerValCysAspLeuAlaValGlnValLeuPheIleLeuAspIleValLeuAsnPhe	279
QY	841	CGIACCACATTCGTGTCCAAAGTCGGGCCAGTGTGTGTGGCCCAAGCCAAAGCCATTGGCTC	900
Db	280	ArgThrThrPheValSerLysSerGlyGlnValValPheAlaProLysSerIleLysLeu	299
QY	901	CACATACGTACACACTGGTCTCTGCTGTGATGTCAATGCAGCCGCTCCCTTGACCTGCTA	960
Db	300	HisTyrValThrThrTrpPheLeuLeuAspValIleAlaAlaLeuProPheAspLeuLeu	319
QY	961	CATGCGTTCAGGTCAGCTGTACTTCGGGGCCCATTCGTGTGAAGACGGTGGCCTGCTG	1020
Db	320	HisAlaPheLysValAsnValTyrPheGlyAlaHisLeuLeuLysThrValArgLeuLeu	339
QY	1021	CGCCTGTGCGCCCTTCCTCCGGGGGTGACCGGTACTCGGACTACAGCGCCGTGGCTGTG	1080
Db	340	ArgLeuLeuAlaGlyLeuLeuProArgLeuAspArgTyrSerGlnTyrSerAlaValAlaValLeu	359
QY	1081	ACACTGCTCATGGCCGTGTTCCCTGCGCTGTCGCGACTGGGCGCTGGCTGGCTGGTTTAC	1140
Db	360	ThrLeuLeuMetAlaValAlaPheAlaLeuLeuAlaHisThrValAlaLysValAlaTrpPheTyr	379
QY	1141	ATTGGCCAGCGCGGAGATCGAGAGCAGCGAATCCAGAGTGCCTGATGTGGCTGGCTCGAG	1200
Db	380	IleGlyGlnArgGlnIleGlnLysSerGlnSerLysLeuProGlnIleGlyTyrPheGln	399
QY	1201	GAGTGGCCGCGCCACTGGAGACTCTCTACTACTGCTGGTGGCGCGAGCCAGCTGAGGCG	1260
Db	400	GlnLeuAlaArgAlaGlyLeuGlnThrProTyrTyrLeuValGlyArgProAlaGlyGly	419
QY	1261	AACAGCTCCGCGCAGAGTGAACAACACTGGAGAGCAGCAGCAGCGCAACGGGAGCGGCTG	1320
Db	420	AsnSerSerLysGlnSerAspAsnLysSerSerSerSerGlnAlaAsnGlyThrGlyLeu	439
QY	1321	GAGCTGCTGGCGGCGCCGTGCTGGCGGAGCGCTTACTACCTCCCTTACTTCGCACTC	1380
Db	440	GlnLeuLeuGlnGlyProSerLeuAlaGlySerAlaTyrIleThrSerLeuTyrPheAlaLeu	459
QY	1381	AGCAGCCTCACAGCGCTGGCTTGGCAACGTTCGCGCAACCGGACCCGAGAGATC	1440
Db	460	SerSerLeuThrSerValGlyPheGlyAsnValSerAlaAsnThrAspThrGlyLysIle	479
QY	1441	TTCTGCATGTGACCATCTCTCATCGCGCCCTGATGCACGCGGTGTGTTTGGAGACGTG	1500
Db	480	PheSerIleLysThrMetLeuIleGlyAlaLeuMetHisAlaValAlaPheGlyAsnVal	499
QY	1501	ACGGCCATATCCAGGGCATGTACGGCCCGCGCTTCTGTACACAGCGGCGCGCAC	1560
Db	500	ThrAlaIleIleIleLysThrMetTyrAlaAlaGArgPheLeuTyrHisSerArgThrArgAsp	519
QY	1561	CTGCGGACATACATCCGATCCACCGTATCCCAAGCCCTTAACGAGCGCATGCTGGAG	1620
Db	520	GlnArgAspTyrIleArgIleHisArgIleProLysProLeuLysGlnArgMetLeuGln	539
QY	1621	TACTTCCAGGGCACCTGGCGGCTGGAACAATGATGCATGCACACACCGAGACTGCTGAGAC	1680
Db	540	TyrPheGlnAlaThrThrPalaValAsnAsnGlyIleAspThrThrGlnLeuLeuGlnSer	559
QY	1681	CTCCCTGAACAGCTGCGCGCAGACATCCCATGCATGCACATGACGAGAGGCTCTGTGAGTGG	1740

472 GCACGATCCAAAGGCTTCAATGCCAACCGGCGGAGCGGCGGCTGTACCACTG 531
200 Ala-----GlycysAsnMetGlyArgArgArgSerArgAlaValLeuTyrGlnLeu 216
532 TCCGGGACACTGCAGAACGAGCCCAAGGCG--AACGCAAGACTCAATTAAGGCG-- 582
217 SerGlyHisTyrLysProGlnLysGlyValLysThrLysLeuLysLeuGlyAsnAsn 236
583 ---GTGTTGGGAGAAACCAAACTTCCCTGAGTCAAAAGTACGCCCATCCGGAACTCG 639
237 PheMetHisSerThrGlnAlaProPheProGlnTyrLysThrGlnSerIleLysLysSer 256
640 CCGTTCATCTGTGACACTGTGGGAGCACTAGAGCCACCGGAGTGGCTTCACTCTGCTC 699
257 ArgLeuIleLeuProHisTyrGlyValPheLysGlyIleThrAspArgValIleLeuVal 276
700 GCCACACTATGTGCTGCTCACTGCTCACTGAGCGGTGTGTGTGAGCAACAGACGGAG 759
277 AlaThrPheTyrValAlaLeuMetValProTyrAsnAlaAlaPheAlaLysAlaAspArg 296
760 CCCAGTCCCGCCCGCGCCGCCAGCGCTGTGACCTGGCGCTGGAGGTCTCTTCAATC 819
297 GlnThr-----LysValSerAspValIleValGlnAlaLeuPheIle 310
820 CTGACATGTGTGCTGAATTCGCTACACATTCGTGTCCAGTGGCGGAGGTGTGTGT 879
311 ValAspIleLeuMetAsnPheArgThrThrPheValSerArgLysGlyValValSer 330
880 GCCCAAAAGTCAATTCGCTCACTGACATGACATGCTGCTGCTGCTGCTGCTGCTGCTG 939
331 AsnSerLysGlnIleAlaIleAsnTyrLeuArgGlyTyrPheAlaLeuAspLeuAla 950
940 GCGCTGCGCTTGTGACCTGTACATGCTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 990
351 AlaLeuProPheAsp-----HisLeuTyrAlaSerAspLeuTyrAspLysGlnAspSer 368
991 ---GCCCATGTGCTGACAGAGGTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1047
369 HisIleHisLeuValLysLeuThrArgLeuMetAlaArgLeuMetLysIle 388
1048 GACCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1107
389 AspArgTyrSerGlnHisThrAlaMetIleLeuThrIleLeuMetPheSerPheThrLeu 408
1108 CTGCGGCACTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1167
409 AlaAlaHisThrPheLeuAlaCysIleThrTyrValIleAlaValLysGlyTyrGln 426
1168 GAATCCGAGCTGCTGAG-----ATTGGGTGGGTCAGAGAGCTGCGCCCGGACTGGAG 1221
427 -----TrpPheProGlnSerAsnIleGlyTyrLeuGlnLeuAlaGlnArg 442
1222 ACTCCCTACTACTGTGTGGCGGAGCGCACTGGAGGAGAACAGCTCGGCGCAAGTGCAC 1281
442 ----- 442
1282 AACTGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 1341
443 -----LysAsnAlaSerValAlaIleLeuThrAlaGln 454
1342 CTGGGAGCGGCTTCACTCACTCCCTCACTCACTCACTCACTCACTCACTCACTCACTG 1401
455 -----ThrTyrSerThrAlaLeuTyrPheThrPheThrSerLeuThrSerValGly 471
1402 TTGGCAAGCTGTGCGCAACAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCTC 1461
472 PheGlyAsnValSerAlaAsnThrThrAlaGlnLysValPheThrIleIleMetMetLeu 491
1462 ATCGGCGCGCTGTATGCAAGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1521
492 IleGlyAlaLeuMetHisAlaValValPheGlyAsnValThrAlaIleIleGlnArgMet 511
1522 TACGCGCGCGCGCTTGTGTACACAGCGGAGCGGCGGAGCTGGCGGACTACATCCGATC 1581

512 TyrSerArgArgSerLeuTyrGlnLysLysTyrPheArgPheLeuLysAspPheValAlaLeu 531
1582 CACGGTATCCCAAGCGCCCTTAACAGAGCGCATGCTGAGTACTTCCAGCGCCACTGGGCG 1641
532 HisAsnMetProLysGlnLeuLysGlnArgIleGlnLysPyrPheGlnThrSerThrSer 551
1642 GTGAAACATGGCAATCGAACACAGCGAGCTGTGTGAGAACCTTCCCTGAGAGACTCCGGCA 1701
552 LeuSerHisGlyIleAspIleTyrGlnThrLeuArgLysPheProGlnGlnLeuArgGly 571
1702 GACATCCCATGCACTGCAACAGAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 1761
572 AspValSerMetHisLeuHisArgGlnIleLeuMetLeuProIlePheGlnAlaAlaSer 591
1762 CCGGCGTGTGCGCGGAGCTGTCTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGGAG 1821
592 GlnGlyLysLeuLysLeuLeuSerLeuHisIleLysThrAsnPheCysAlaProGlyGln 611
1822 TACCTATCCACAAAGCGATGCGCTGCAAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1881
612 TyrLeuIleHisLysGlyAspAlaLeuAsnTyrIleTyrTyrLeuLysAsnGlySerMet 631
1882 GAGGTGTCAAGGCTGCGACCGCTGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1941
632 GlnValIleLysAspAspMetValAlaIleLeuGlnLysGlyLysPheValGlySer 651
1942 GACCTG----- 1947
652 AspIleAsnValHisLeuValAlaThrSerAsnGlyGlnMetThrAlaThrThrAsnSer 671
1948 CCGCGCGGAGAGCGAGTGTGTAAGGCCAATCCGAGCTGTAAGGCGGTGAGCTGCTGCTC 2007
672 AlaGlyLysAspValValValArgSerSerSerAspIleLysAlaLeuThrTyrCysAsp 691
2008 CTGCACTGTGCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2067
692 LeuLysCysIleHisMetLysGlyLeuValGlnValLeuArgLeuTyrProGlnTyrGln 711
2068 CCGCGCTTACGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2127
712 GlnGlnPheAlaAsnAspIleGlnHisAspLeuThrCysAsnLeuArgGlnGlyTyrGln 731
2128 TCTGCAAGAGTGAACAGCAGC-----TCTGAGCGGCGCAATACC 2169
732 AsnGlnAspSerAspIleGlyProSerPheProLeuProSerIleSerLysAspArg 751
2170 CTATATGCCACGCTGAG-----GAGAGGAGACAGATGGGAGAGCGAGCGC 2214
752 AsnArgGlnGlnAlaGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 769
2215 CCC-----ACGCTCTCCCAAGCCCAAGCTGATGAGCGCTCC 2250
770 ProProSerGlyAlaSerProLeuHisAsnIleSerAsnSerProLeuHisAlaThrArg 789
2251 AGCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2310
790 SerProLeuLeuGlyMetGly-----SerPro 798
2311 CGTGCACAGACACCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2370
799 Arg-----AsnGlnArgLeuHisGlnAlaGly 807
2371 TTGAAGCTGAGGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2430
808 -----ArgSerLeuIleThrLeuArg----- 814
2431 CCGATGCCAATGAATGTGCCCGAGATGTGAGCCCGAGAGTGAATGAGATGAGATGAGAGAC 2490
815 -----GlnThrAsnLysArgHisArgThrLeuAsnAla----- 825
2491 GCGTGTGCTGCGACCAAGCCCAAGTCTCTTCCGCGGTGGCGAGTGTGCGCGGAATGT 2550

Db 826 AlaCysSerLeuAspArgGlySerPhe----- 834
QY 2551 AGCAGACACCCCTCCCTGGAGACAGAGCCGCTGTCACGTTCCTCCATGGGCCAGC 2610
Db 835 ---GluGluProGluProLeuGluGluGlu-----GlnSer 845
QY 2611 GAGGAGAGGAACAGACAGACTGGACAGACTTCGGACAGCGGTGACAGAGCTGTACAG 2670
Db 846 SerGlyGlyLysArgProSerLeuGluArgLeuAspSerGlnValSerThrLeuHisGln 865
QY 2671 CAGGTGCTGCAGATCGGGAGAGAGACTGACATTCGGACAGCGGTGACAGCTGTCTCTG 2730
Db 866 AspValAlaGlnLeuSerLeuGluValAlaArgAsnAlaIleSerAlaLeuGlnGluMet--- 884
QY 2731 GCGCCACAGAGGAGGAGGTCGCTGCCCTCGGCATCGGAGAGGCGCGTCCAGCAGCAG 2790
Db 885 -----ThrPhe 886
QY 2791 ACCTCGGGCTTCTGCAGCCTGTGTGTGACACTGGGGACATTCCTACTGCTCGCAG 2850
Db 887 ThrSerAlaMet-----ThrSerHisSerLeuLysPhe--- 899
QY 2851 CCCCCAGCGCTGCTGTC-----TTGAGTGGACTTGGCCACCCCTGCGGGGCGCT 2904
Db 900 ProProAlaArgSerLeuProAsnIleSerGly--ValAlaGlyThrArgSerGlyValAla 919
QY 2905 CCTCCCTCATGAGCAGCTGCGCTGGGCTGCCAGCGCTGACAGCTGCCCTGCGCT 2964
Db 919 AlaAlaGlnHisGlyLeuMetGly---GlyValLeuAlaIleAlaGlnLeu--AlaAlaMet 937
QY 2965 CGAGCCAGACGTTTCTGAGACTTCACCT-----CAGACTCAGAGCCCGCTGCC 3012
Db 937 TglnArgSerSerSerHisArgProGluValAlaTrpGlyArgAspValGlnLeuProThrSe 957
QY 3013 TCAGGAGACTCTGCTGCTGAGCCAGCAGACCCCGCTGCC 3052
Db 957 AsnThrAlaSerSerLysAlaProSerProValGluPro 970

RESULT 7
US-09-119-855-11
; Sequence 11, Application US/09119855
; Patent No. US20020099197A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Roy A.J.
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
; FILE REFERENCE: mnl-055
; CURRENT APPLICATION NUMBER: US/09/119, 855
; CURRENT FILING DATE: 1998-07-21
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 1284
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-119-855-11

Alignment Scores:
Pred. No.: 8,52e-87 Length: 1284
Score: 1901.00 Matches: 455
Percent Similarity: 53.85% Conservative: 146
Best Local Similarity: 40.77% Mismatches: 273
Query Match: 31.22% Indels: 242
DB: 10 Gaps: 31

US-09-965-830-1_COPY_6_3257 (1-3252) x US-09-119-855-11 (1-1284)
QY 1 ATGCGGCGCATCGGGGCTCTGCGGCTCAGAACACCTTCCTGGACATGCTACG 60
Db 1 MetProAlaArgLysGlyLeuAlaProGlnAsnThrPheLeuAspThrIleAlaThr 20
QY 61 CGCTTCGAGCGCAGCAGATTAATCTGCTGCGGCAAGCCGAGTGGCGGCTCTTC 120
Db 21 ArgPheAspGlyThrHisSerAspHeValLeuGlyAsnAlaGlnAlaAsnGly---Asn 39

QY 121 CCGGTGCTACTGCTGTGATGGCTTCTGTGACCTTCAGGCGCTTCCCGGCTAGCTC 180
Db 40 ProIleValIleTyrCysSerAspGlyPheValAlaSerPheThrGlyTyrSerArgAlaGlnIle 59
QY 181 ATGCAGCGGGGCTGTCCTGCTGCTCTTATGGGCCAGACAGCAGTACGCTGCGCC 240
Db 60 MetGlnLysGlyCysSerTyrHisPheLeuTyrGlyProAspThrLysGlnGlnHisLys 79
QY 241 CAACAGATCCGCAAGGCGTGGACAGCAGCAGCAAGAGATTCAAGGCTGAGCTGTAC 300
Db 80 GlnGlnIleGlnLysSerLeuSerAsnLysMetGlnLeuLysLeuGlnValIlePheTyr 99
QY 301 CGAAGAGCGGCTCCCTGCTGCTGCTGCTGATGATGATACCAATGAAGATGAAGA 360
Db 100 LysLysGlnGlyAlaProPheThrPyrCysLeuPheAspIleValProIleLysAsnGlnLys 119
QY 361 GGGAGGTGCTCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 411
Db 120 ArgAspValIleLeuPheLeuAlaSerHisLysAspIleThrHisThrLysMetLeuGln 139
QY 411 ----- 411
Db 140 MetAsnValAsnGlnGluCysAspSerValPheAlaLeuThrAlaAlaLeuGlnGlyAla 159
QY 412 -----AACGAGCG 420
Db 160 ArgPheArgAlaGlySerAsnAlaGlyMetLeuGlyLeuGlyLeuProGlyLeuGly 179
QY 421 GGGCCC-----GACAGATGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 471
Db 180 GlyProAlaAlaSerAspGlyAspThrGlnAlaGlyGlnLysAsnLeuAspValPro 199
QY 472 GCAAGATCAAGAGCTCAATGCCAACCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAG 531
Db 200 Ala-----GlyCysAsnMetGlyArgArgSerArgAlaValAlaLeuTyrGlnLeu 216
QY 532 TCGGGGAGCTGCAAGAGCAGCAGCCCAAGGC---AAGCACAAGCTCAATGAAGGG- 582
Db 217 SerGlyHisTyrLysProGlnLysGlyValLysThrLysLysLeuGlyAsnAsn 236
QY 583 ---GTGTTGGGAGAACCAAACTGCTGAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAG 639
Db 237 PheMetHisSerThrGlnAlaProPheProGluTyrLysThrGlnSerIleLysLysSer 256
QY 640 CCTTCATCCGTGTTGACTGCTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 699
Db 257 ArgLeuIleLeuProHisTyrGlyValPheLysGlyIleTrpAspTrpValIleLeuVal 276
QY 700 GCGACACTATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 759
Db 277 AlaThrPheTyrValAlaLeuMetValProTyrAsnAlaAlaPheAlaLysAspArg 296
QY 760 CCCAGTGGCCCG 819
Db 297 GlnThr-----LysValSerAspValIleValAlaLeuPheIle 310
QY 820 CTTCAGATTCGCTGAATTCGATCCAGACATTCGCTGCTGCTGCTGCTGCTGCTGCT 879
Db 311 ValAspIleLeuLeuAsnPheArgThrThrPheValSerArgLysGlyValValSer 330
QY 880 GCCCAAGGTCATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 939
Db 331 AsnSerLysGlnIleAlaIleAsnTyrLeuArgGlyTrpPheAlaLeuAspLeuAla 350
QY 940 GCGGTGCTTGAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 990
Db 351 AlaLeuProPheAsp-----HisLeuTyrAlaSerAspLeuTyrAspGlyGlnAspSer 368
QY 991 ---GCCCATTCGCTGAG 1047
Db 369 HisIleHisLeuValLysLeuThrArgLeuLeuArgLeuAlaArgLeuLeuGlnLysIle 388

```
OY 1048 GACCGTACTGTCAGTACAGCGCGGCGGCGTGTGACATGCTGTATGCGCGCTGTGCGCTG 1107
|||||
DB 389 AsparagylSerGlnHisThrAlaMetIleuThrIleuMetPheSerPheThrIleu 408
|||||
OY 1108 CTCGGCAGCATGGTGGCGCTGGCTGTGTTTACATTGGCGACGGGAGATGACAGAC 1167
|||||
DB 409 AlaAlaHisThrPheAlaCysIleThrPtyValIleAlaValLysGlnTyGlu 426
|||||
OY 1168 GAATCCGAGCTGCTGAG-----ATTGCTGCTGTCAGAGAGCTGGCGCGGACTGGAG 1221
|||||
DB 427 -----TrpPheProGluSerAsnIleGlyThrPheGlnIleuAlaGluArg----- 442
|||||
OY 1222 ACTCCCTACTACTCTGTGGCGCGGAGCGACCTGTGAGGAACAGCTCCGCCAGAGTGAC 1281
|||||
DB 442 ----- 442
|||||
OY 1282 AACTGACAGACAGCAGGACCCCAAGCGGAGCGGCTGTGAGCTGTGGCGCGCGCTGC 1341
|||||
DB 443 -----LysAsnAlaSerValAlaIleuThrThrAlaGlu----- 454
|||||
OY 1342 CTCGGCAGCGCTTACATCATCTCCCTACTTCCACTGTACAGACCTTACCAGCGTGGC 1401
|||||
DB 455 -----ThyThrSerThrAlaLeuTyPheThrPheThrSerLeuThrSerValGly 471
|||||
OY 1402 TTGGGCAACGTGTCCGCGCAACAGGACAGCAGAGAGATCTTCCATCTGTGACCATGCTC 1461
|||||
DB 472 PheGlyAsnValSerAlaAsnThrThrAlaGluValPheThrIleMetMetIleu 491
|||||
OY 1462 ATGGGGCGCTGTATGACAGCGGTGTGTGTGGACGTGACGCGCATCTGACAGCGCATG 1521
|||||
DB 492 IleGlyAlaLeuMetHisAlaValValPheGlyAsnValThrAlaIleIleGlnArgMet 511
|||||
OY 1522 TAGCGCGCGCGCTTGTGTACACAGCGCGGACCGGAGCGGACTGTGCGACATCATCCGATG 1581
|||||
DB 512 TyrSerArgArgSerLeuTyGluSerLysTrpArgAspLeuLysAspPheValAlaLeu 531
|||||
OY 1582 CACCGTATCCCCAGCGCGCTGTGACAGCGGAGCGGACTGTGAGTCTTCCAGCGCATGCGGCG 1641
|||||
DB 532 HisAsnMetProLysGluLeuLysGlnArgIleGlnAspTyPheIleThrSerTrpSer 551
|||||
OY 1642 GTGACACATGAGCATGACACACACCGAGCTGTGACAGCGCTCCCTGACAGCATGCGCGCA 1701
|||||
DB 552 LeuSerHisGlyIleAspIleTyGluThrLeuArgGluPheProLysGluLeuArgGly 571
|||||
OY 1702 GACATCGCGCATCTGACAGAGAGTCTGTGACGCTGCTGCTGTGAGCGCGGCGCAG 1761
|||||
DB 572 AspValSerMetHisLeuHisArgGluIleLeuGlnLeuProIlePheGlnAlaAlaSer 591
|||||
OY 1762 GCGCGCTGCTGCGCGGCTGTCTGTGCGCTGTGCGCGCGCTGTGTGACGCGCGGCGAG 1821
|||||
DB 592 GlnGlyCysLeuLysLeuSerLeuHisIleLysThrAsnPheCysAlaProGlyGlu 611
|||||
OY 1822 TACCATTCACACAGGAGGATGCGCTGTGAGCGCTGTGCTGTGCTGTGCTGTGCTG 1881
|||||
DB 612 TyrIleuIleHisLysGlyAspAlaLeuAsnTyIleTyTyLeuCysAsnIleYerMet 631
|||||
OY 1882 GAGGTGTCAAGGAGGTCGCTGCTGCGCATCTCCAGGAGGAGGCGGAGCTGTATCGGCTGT 1941
|||||
DB 632 GluValIleLysAspAspMetValValAlaIleLeuGlyLysGlyAspLeuValGlySer 651
|||||
OY 1942 GAGCTG----- 1947
|||||
DB 652 AspIleAsnValHisLeuValAlaThrSerAsnGlyGlnMetThrAlaThrThrAsnSer 671
|||||
OY 1948 CCGCGGGGGAGGAGGTGTGTAAGGCCATGCCAGCTGAAGGGGCTGACCTACTGCTGC 2007
|||||
DB 672 AlaGlyIleAspValValValArgSerSerSerAspIleLysAlaLeuThrThrCysAsp 691
|||||
OY 2008 CTGAGAGTGTGAGCGTGGCGCTGCTGACAGACAGCTGTGCGCTGTACCCCGAGATTGGCC 2067
|||||
DB 692 LeuLysCysIleHisMetGlyGlyLeuValGlyValIleuArgLysTyProGluTyGln 711
|||||
OY 2068 CCGCGCTTCACTGTGCTCCGAGGGGAGCTGACACAACTGGGCTGCTGGGGGAGCG 2127
|||||

DB 712 GlnGlnPheAlaAsnAspIleGlnHisAspLeuThrCysAsnLeuArgGluTyGlu 731
|||||
OY 2128 TCTGACAGAGTGAACACAGC-----TCTGAGCGCGCGCACATACC 2169
|||||
DB 732 AsnGlnAspSerAspIleGlyProSerPheProLeuProSerIleSerGluAspArgGlu 751
|||||
OY 2170 CTTATGTCACGCTGAG-----GAGAGAGACAGATGAGGAGGAGCGG 2214
|||||
DB 752 AsnArgGluAlaGlnGluGluGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 769
|||||
OY 2215 CCC-----ACGCTCTCCACCGCCGAGCTGATGAGCGCTCC 2250
|||||
DB 770 ProProSerGlyAlaSerProLeuHisAsnIleSerAsnSerProLeuHisAlaThrArg 789
|||||
OY 2251 AGCCCCGCTGTGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2310
|||||
DB 790 SerProLeuLysGlyMetGly-----SerPro 798
|||||
OY 2311 CGTGCACAGCAGCAGCCCGGCTGTCTAGTGTGACAGAGGAGGAGCAGGAGGAGGCT 2370
|||||
DB 799 Arg-----AsnGlnArgLeuHisGlnArgGly----- 807
|||||
OY 2371 TTGAAGCTGAGGCTGGCGCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2430
|||||
DB 808 -----ArgSerLeuIleThrLeuArg----- 814
|||||
OY 2431 CCGATGCCATGAGATGTGCCCGCCAGATCTGAGCCCGAGGAGGAGTGAATGATGAGAC 2490
|||||
DB 815 -----GluThrAsnLysArgHisArgThrLeuAsnAla----- 825
|||||
OY 2491 GCGTGTGCTGCGACACAGCCAGCTGTCTTCCGCGTGGCGGAGTGTGCGCGGAGTGT 2550
|||||
DB 826 AlaCysSerLeuAspArgGlySerPhe----- 834
|||||
OY 2551 AGCAGCAGCGCCCGCTGCGACAGAGAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2610
|||||
DB 835 -----GluGluProGluProLeuGluGluGlu-----GlnSer 845
|||||
OY 2611 GAGCGAAGGACACAGACACACTGTGACAGCTTCCGCGAGCGGTGACAGCTGTACAG 2670
|||||
DB 846 SerGlyGlyLysArgProSerLeuGluAlaGlyLeuAspSerGlnValSerThrLeuHisGln 865
|||||
OY 2671 CAGTGTGCTGACAGTGGGAGGAGTCACTGTGCGGAGGAGGAGGAGGAGGAGGAGGAG 2730
|||||
DB 866 AspValAlaGlnLeuSerHisAlaGluValArgAsnAlaIleSerAlaLeuGlnGluMet 884
|||||
OY 2731 GCGCGCCACAGGAGGAGGCTGCTGCTGCGGAGATCGGAGAGGCGCTGCGCAGCGAG 2790
|||||
DB 885 -----ThrPhe 886
|||||
OY 2791 ACTCGCGGCTTGTGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2850
|||||
DB 887 ThrSerAsnAlaMet-----ThrSerHisSerLeuLysPhe----- 899
|||||
OY 2851 CCGCCAGCTGTGCTGCT-----TTGAGTGGAGCTGTGCGCGCGCGCGCGCT 2904
|||||
DB 900 ProProAlaArgSerIleLeuProAsnIleSerGly--ValAlaGlyThrArgSerGlyVal 919
|||||
OY 2905 CCGCCCTGAGGAGCAGCTGTGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 2964
|||||
DB 919 IlaValGlnHisGlyLeuMetGly--GlyValLeuAlaAlaIleu--AlaAlaMet 937
|||||
OY 2965 GAGCGACAGCTTGTGTGACCTCACT-----CAGACTCAGAGCGCGCGCTGCC 3012
|||||
DB 937 GlnArgSerSerSerHisProProGluValIleProLysArgAspValGlnLeuProThr 957
|||||
OY 3013 TCAGAGACCTGTGCTGTGAGCCAGCAGCAGCTGCTGCTGCC 3052
|||||
DB 957 AsnThrAlaSerSerLysAlaProSerProValGluPro 970
|||||

RESULT 8
US-09-119-855-5
```


FILE REFERENCE: Vanderbilt Ref No. US2003001336A1 V0120; Attorney Docket No. US2003
CURRENT APPLICATION NUMBER: US/10/000,151B
CURRENT FILING DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 1159
TYPE: PRT
ORGANISM: Homo sapiens
US-10-000-151B-3

Alignment Scores:
Pred. No.: 1.83e-69 Length: 1159
Score: 1551.00 Matches: 424
Percent Similarity: 44.86% Conservative: 143
Best Local Similarity: 33.54% Mismatches: 337
Query Match: 25.47% Indels: 360
DB: 9 Gaps: 38

US-09-965-830-1_COPY_6_3257 (1-3252) x US-10-000-151B-3 (1-1159)

QY 1 ATGCCGCGCATATGCGGCGCTCTGCGCTCAGAACACCTTCGTGACACCATCGCTACG 60
Db 1 MetProValArgArgGlyHisValAlaProGlnAsnThrPheLeuAspThrIleIleArg 20
QY 61 CGCTTCAGCGCAGCAGCAGTAACTGCTGCGTGGCAACGCCAGGCGCGGCTCTTC 120
Db 21 LysPheGluGlnSerArgLysPheIleIleAsnAlaArgValGluAsnGly 39
QY 121 CCGGTGTCTACTGCTCTGTATGCTTCTGACCTCAGCGCTTCCTCCGCGGTGAGTC 180
Db 40 AlaValIleTyrCysAsnAspGlyPheCysGluLeuGlyTyrSerArgAlaGluVal 59
QY 181 ATGCAGCGGCGCTGCT 240
Db 60 MetGlnArgProCysThrCysAspPheLeuHisGlyProArgThrGlnArgAlaAla 79
QY 241 CAACAGATCCGACAGCGCTCGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 300
Db 80 AlaGlnIleAlaGlnAlaLeuLeuGlyAlaGluGlnArgValGluIleAlaPheTyr 99
QY 301 CGGAGAGCGGCTCCGCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 360
Db 100 ArgLysAspGlySerCysPheLeuGlyValAspValAlaProValLysAsnGluAsp 119
QY 361 GGGGAGGTGGCT 399
Db 120 GlyAlaValIleMetPheIleLeuAsnPheGluValAlaMetGluLysAspMetValGly 139
QY 400 AGGAAACCAAGACGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 435
Db 140 SerProAlaHisAspThrAsnHisArgGlyProProThrSerThrPheAlaProGlyArg 159
QY 435 435
Db 160 AlaIysThrPheAlaGlyLeuLysLeuProAlaLeuLeuAlaLeuThrAlaArgGluSerSer 179
QY 436 AAGGAGACAGGTGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 489
Db 180 ValArgSerGlyGlyAlaGly-GlyAlaGlyAla-ProGlyAlaValAlaValAspVala 199
QY 490 AATGCCAACCG 503
Db 199 SplenThrProAlaAlaProSerSerGluSerLeuAlaLeuAspGluValThrAlaMet 219
QY 504 504
Db 219 SpAsnHisValAlaGlyLeuGlyProAlaGluGluArgAlaLeuValGlyProGly 239
QY 525 CCACCTGTCCGGGACCTTCGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 576
Db 239 eTProProArgSerAlaProGlyGlnLeu-ProSerProArgAlaHisSerLeuAsnPro 258

QY 576 576
Db 259 AspAlaSerGlySerSerCysSerLeuAlaArgThrArgSerArgGluSerCysAlaSer 278
QY 577 577
Db 279 ValArgArgAlaSerSerAlaAspAspIleGluAlaMetArgAlaGlyValLeuProPro 298
QY 595 AAACCAAC 603
Db 299 ProProArgHisAlaSerThrGlyAlaMetHisProLeuArgSerGlyLeuLeuAsnSer 318
QY 603 603
Db 319 ThrSerAspSerAspLeuValArgTyrArgThrIleSerLysIleProGlnIleThrLeu 338
QY 603 603
Db 339 AsnPheValAspLeuLysGlyAspProPheLeuAlaSerProThrSerAspArgLulle 358
QY 603 603
Db 359 IleAlaProLysIleLysGluArgThrHisAsnValThrGluLysValThrGlnValLeu 378
QY 604 604
Db 379 SerLeuGlyAlaAspValLeuProGluTyrLysLeuGlnAlaProArgIleHisArgTyr 398
QY 646 ATCCGTGTCAGCTGCGGCGCGCTGAGAGCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 705
Db 399 ThrIleLeuHisTyrSerProPheLysAlaValIleTrpAspThrLeuIleLeuLeuVal 418
QY 706 CTCTATGTGCTGTCTACTGCTGCTCTGACAGCGCTGTGTGTG 756
Db 419 IleThrAlaValAlaPheThrProTyrSerAlaAlaPheLeuLeuLysGluThrGluGlu 438
QY 757 GAGCCAGTGCC 801
Db 439 GlyProProAlaThrGluLysGlyTyrAlaCysGlnProLeuAlaValAlaAspLeuIle 458
QY 802 GTGAGGCT 861
Db 459 ValAspLeuPheIleValAspIleLeuIleAsnPheArgThrThrIleValAsnAla 478
QY 862 TCGGCGCAGGTGTGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 921
Db 479 AsnGluGlnValValSerHisProGlyArgIleAlaValHisTyrPheLysGlyTyrPhe 498
QY 922 CTGCTGATGATCATCGACGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 981
Db 499 LeuIleAspMetValAlaAlaIleProPheAspLeu 511
QY 982 TACTTCGGGCGC 1023
Db 512 IlePheGlySerGlySerGluGluLeuIleGlyLeuLeuLysThrAlaArgLeuLeuArg 531
QY 1024 CTGCTGCGCT 1083
Db 532 LeuValArgValAlaArgLysLeuAspArgTyrSerGluTyrGlyAlaAlaValLeuPhe 551
QY 1084 CTGCTCAGGCGGTGTGGCGCGCGCTGCGCGCGCTGCGCGCGCTGCGCTGCTTACAT 1143
Db 552 LeuLeuMetCysThrPheAlaLeuIleAlaHisThrPheAlaLysIleTyrPylAlaIle 571
QY 1144 GCGCAGCGGAGATCGAGACGAGGAAATCGAGCTGCTGAGATTCGTGCTGCTGCGAG 1203
Db 572 GlyAsnMetGluGlnProHisMetAspSer-ArgIleGlyTyrPheHisAsn 588
QY 1204 CTGCGCGCGGACGTGAGACTCCCTACTACTGTGTGGCGCGGAGCCAGCTGAGGAG 1263
Db 589 LeuGlyAspGlnIleGlyLysProTyr-Asn 598
QY 1264 AGCTCGCGCCAGAGTCAACACTGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1323

ORGANISM: Homo sapiens
US-10-193-692-5

Alignment Scores:

Pred. No.: 1,83e-69 Length: 1159
Score: 1551.00 Matches: 424
Percent Similarity: 44.86% Conservative: 143
Best Local Similarity: 33.54% Mismatches: 337
Query Match: 25.47% Indels: 360
DB: 9 Gaps: 38

US-09-965-830-1_COPY_6_3257 (1-3252) x US-10-193-692-5 (1-1159)

```

QY 1 ATCCGGCCCATCGGGGCTCTGCGCCCTCAGAACACCTTCTGGACACCATCGCTACG 60
Db 1 MetProValArgArgGlyHisValAlaProGlnAsnThrPheLeuAspThrIleLeuArg 20
QY 61 CCCTTGACGCGACGACAGTACTTCTGCTGGCAGCCCGCAGGGGCGGCTCTTC 120
Db 21 LysPheGlnGlyGlnSerArgPheIleIleAlaAsnAlaArgValGlnAsnGly 39
QY 121 CCCGGTCTACTGCTCTATGCTGTCTGTGACTCAGCGGCTTCCCGGCTGAGTC 180
Db 40 AlaValIleTyrCysAsnAspGlyPheCysGlyLeuGlyTyrSerArgAlaGlyVal 59
QY 181 ATGACGCGGGGCTGTGCTCTCTCTCTCTTATGGCCAGACAGCAGTGGCTCGCCG 240
Db 60 MetGlnArgProCysThrCysAspPheLeuHisGlyProArgThrGlnArgAlaAla 79
QY 241 CAACAGATCCGACAGGCGCTGACGACGACAGGAGTTCAGGCTGACCTGATCTGAC 300
Db 80 AlaGlnIleAlaGlnAlaLeuLeuGlyValAlaGlnGlnArgValGlnIleAlaPheTyr 99
QY 301 CGGAGACGCGGCTCCGCTTCTGTCTCTGATGATGATGATGATGATGATGATGATG 360
Db 100 ArgGlyAspGlySerCysPheLeuGlyValAlaValAlaProValGlyAsnGlnLys 119
QY 361 GGGGAGTGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 399
Db 120 GlnValAlaIleMetPheIleLeuAsnPheGlnValAlaMetGlyLysAspMetValGly 139
QY 400 ---AGGAAACCAACAGAACCCAGGCGGCGCCGACAGATGG--- 435
Db 140 SerProAlaHisAspThrAsnHisArgGlyProProThrSerThrPheLeuAlaProGlyArg 159
QY 435 --- 435
Db 160 AlaIysThrPheArgLeuLysLeuProAlaLeuLeuAlaLeuThrAlaArgLysSer 179
QY 436 ---AAGGAGACAGGTGGTGGCGCGCGCGATATGCGCGGCG---ACGATCCAAAGGCTTC 489
Db 180 ValArgSerGlyGlyAlaGlyGlyAlaGlyAlaGlyAlaGlyAlaGlyAlaGlyAla 199
QY 490 AATGCCAACCGCGCG--- 503
Db 199 splLeuThrProAlaAlaProSerSerGlnSerLeuAlaLeuAspGlnValThrAlaMet 219
QY 504 ---GCGGAGCCGCGCGCTGCTCTA--- 524
Db 219 spAsnHisValAlaGlyLeuGlyProAlaGlnGlnArgArgAlaLeuValGlyProGly 239
QY 525 ---CCACCTGTCGCGGCGACCTGACAGAACGACCCAAAGGCGCAG---CACAAAGCTCAAT--- 576
Db 239 erProProArgSerAlaProGlyGlnLeu-ProSerProArgAlaHisSerLeuAsnPro 258
QY 576 --- 576
Db 259 AspIaSerGlySerSerCysSerLeuAlaArgThrArgSerArgLysSerCysAlaSer 278
QY 577 ---AAGGGGCTTTGGGAG 594
Db 279 ValArgArgAlaSerSerAlaAspAspIleGlnAlaMetArgAlaGlyValLeuProPro 298

```

```

QY 595 AAACCAAC----- 603
Db 299 ProProArgHisAlaSerThrGlyAlaMetHisProLeuArgSerGlyLeuLeuAsnSer 318
QY 603 ----- 603
Db 319 ThrSerAspSerAspLeuValArgTyrArgThrIleSerLysIleProGlnIleThrLeu 338
QY 603 ----- 603
Db 339 AsnPheValAspLeuLysGlyAspProPheLeuAlaSerProThrSerAspArgGlnIle 358
QY 603 ----- 603
Db 359 IleAlaProLysIleLysGlnArgThrHisAsnValThrGlnLysValThrGlnValLeu 378
QY 604 -----TTCCTGACTACAAAGTACCGCCATCCGAGAGTGGCTTC 645
Db 379 SerLeuGlyAlaAspValLeuProGlnLysLeuGlnAlaProArgIleHisArgTyr 398
QY 646 ATCTGTGACGCTGGGGGCGACAGACGACACCTGGGATGGCTTACATCTGCTGGCACA 705
Db 399 ThrIleLeuHisTyrSerProPheLysAlaValAlaTyrAspThrPheLeuLeuLeuVal 418
QY 706 CTCTATGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 756
Db 419 IleTyrThrAlaValPheThrProTyrSerAlaAlaPheLeuLeuLysGlnThrGlnGln 438
QY 757 GAGCCCAAGTGC-----GCCCGCGCGCGCCGACGCTGTGACCTGGCC 801
Db 439 GlyProProAlaThrGlnLysGlyTyrAlaCysGlnProLeuAlaValAlaAspLeuIle 458
QY 802 GTGGAGGCTCTTATCTGATCTGATGATGATGATGATGATGATGATGATGATGATG 861
Db 459 ValAspIleMetPheIleValAspIleLeuLeuAsnPheAspGlyThrTyrAlaAsnAla 478
QY 862 TCGGCGCAGGCGGCTTGGCCCAAGTCATTTGCTCCACTACGACACCTGCTGCTG 921
Db 479 AsnGlnGlnValIleSerHisProGlyArgIleAlaValHisTyrPheLysGlyTyrPhe 498
QY 922 CTGCTGATGTCATCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 981
Db 499 LeuIleAspMetValAlaAlaIleProPheAspLeuLeu----- 511
QY 982 TACTTGGGGCC-----CATGCTGAAGACGCTGCGCTGCTGCGC 1023
Db 512 IlePheLysSerGlySerGlnGlnLeuIleLysLeuLeuLysThrAlaArgLeuLeuArg 531
QY 1024 CTGCTGCGCTGCTTCCGCGCTGACGCGGTACCGAGTACAGCGCGCGGTGCTGACA 1083
Db 532 LeuValArgValAlaArgLysLeuAspArgTyrSerLysGlyAlaAlaValLeuPhe 551
QY 1084 CTGCTGATGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1143
Db 552 LeuLeuMetCysThrPheAlaLeuIleAlaHisThrLeuAlaLysIleThrPyrAlaIle 571
QY 1144 GGCACAGCGGAGTGCAGAGCAGACGACGATCCGAGTCTGATGATGCTGCTGCGAGAG 1203
Db 572 GlnAsnMetGlnGlnProHisMetAspSer-----ArgIleLysThrPheLeuHisAsn 588
QY 1204 CTGGCGCGCGGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 1263
Db 589 LeuGlyAspGlnIleGlyLysProTyr-----Asn 598
QY 1264 AGCTCCGCGCAGAGTACAGACGACGACGACGACGACGACGACGACGACGACGACG 1323
Db 599 SerSerGly----- 601
QY 1324 CTGCTGGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1383
Db 602 ---LeuGlyGlyProSerIleLysAspLysTyrAlaThrAlaLeuTyrPheThrPheSer 620
QY 1384 AGCTCAACACGCGGCTTGGCAGCTGTGCGCCAAACAGGACGACGACGACGACGACGATCTTC 1443

```

|||||
Db 621 SerLeuThrSerValGlyPheGlyLysValSerProAsnThrAsnSerGlnLysIlePhe 640
1444 TCACATGTCACCATGTCATGGGCGCCCTGATGACAGCGGCTGTGTGGAGACCTGACG 1503
|||||
Db 661 SerIleCysValMetLeuIleGlySerLeuMetValSerIlePheGlyAsnValSer 660
1504 GGCATCATCCAGCGCATGACGCGCGCGCTTCTGTACACAGCGGACGCGGACCTG 1563
|||||
Db 661 AlaIleIleGlnValLeuLysSerGlyThrAlaArgTyrHisThrGlnMetLeuArgVal 680
1564 GCGCATCATCCGCGCATCCGCTATCCGCGCGCTGACAGCGGCTGACGCGGCTGAC 1623
|||||
Db 681 ArgGluPheIleArgPheHisGlnIleProAsnProLeuArgGlnArgLeuGlnGlyTyr 700
1624 TTCAGGCGCGCATCGGCGGCTGAAACATGCGCATCGACACAGGAGGCTGCGAGCTC 1683
|||||
Db 701 PheGlnHisAlaIleTrpSerGlyTyrHisGlnGlyIleAspMetAsnAlaValLeuLysGlyPhe 720
1684 CCTGACGACCTGCGCGCGCGCATCGCGCATCGACACAGGAGGCTGCGAGCTG 1740
|||||
Db 721 ProGlnCysLeuIleAlaSerIleCysLeuHisLeuAsnArgSerLeuLeuGlnHisCys 740
1741 CCACTGTTGAGCGCGCGCGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTG 1800
|||||
Db 741 LysProPheArgGlyAlaThrLysGlyCysLeuArgAlaLeuAlaMetLysPheLysThr 760
1801 GCGTTCGACGCGCGCGCGCGCTGACCTCATCCACAGCGGCTGCGCGCTGCGCGCTTAC 1860
|||||
Db 761 ThrHisAlaProProGlyArgPheThrLeuValHisAlaGlyAspLeuLeuThrAlaLeuTyr 780
1861 TTGTGCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1920
|||||
Db 781 PheIleSerArgLysSerIleGlnIleLeuArgLysValValAlaAlaIleLeuGly 800
1921 AAGGCGCACTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1980
|||||
Db 801 LysAsnAspIlePheGlyGluProLeuAsnLeuTyrAlaArgProGlyLysSerAsnLys 820
1981 GACGTGAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2040
|||||
Db 821 AspValAlaGlnLeuThrTyrCysAspLeuHisLysIleHisArgAspAspLeuGln 840
2041 AGCCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2100
|||||
Db 841 ValLeuAspMetTyrProGlnPheSerAspHisPheTrpSerLeu 858
2101 AGCTACAACTG 2142
|||||
Db 859 ThrPheAsnLeuAlaArgAspThrAsnMetIleProGlySerProGlySerThrGlnLeuGln 878
2143 ACCAGCTCCCTGAGCGCGCACATACCTTATGTCACGCTGAGGAGAGAGACAGAT 2202
|||||
Db 879 GlyGlyPheSerArgLysArgLysArgLysLeuSerPheArgArgArgThrAspLysAsp 898
2203 GGGGACAGAGGCGCGCGCGCTCCCGACGCGCGCTGATGAGCCTCCAGCCCTGCTG 2262
|||||
Db 899 ThrGlnGln 901
2263 TCCCGTGGCTGACCTCCATCTCATCTGCTGCAAGCTGCTATCCCGACGCTGCAACGCA 2322
|||||
Db 902 ---ProGlyGlnValSerAla 914
2323 CCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2382
|||||
Db 915 AlaGlyPro 932
2383 GCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2418
|||||
Db 933 SerGlyProSerSerProGlnSerSerGlnAspGlnGlyProGlyArgSerSerSerPro 952
2419 CTAGGCTG 2466
|||||

Db 953 LeuArgLeuValProPheSerSerProArgProProGlyGluProProGlyGluPro 972
2467 AGGGTAGTAGATGGCATTTGAAGACGGCTGTGCTGGACACGCGCAAG 2514
973 ---LeuMetGlnAspCysGlnLysSerSerAspThrCysAsnProLeuSerGlyAlaPhe 991
2515 ---TTCCTTTC 2538
Db 992 SerGlyValSerAsnIlePheSerPheTrpGlyAspSerArgGlyArgGlnLysGln 1011
2539 GCGCGGAGATGTAGACAGCGCGCTCCCTGGACCGACAGAGCGGCTGCTGCTGCTGCTGCTG 2595
1012 LeuProArgCys 1026
2596 ---CCCATGGCG 2634
1027 LeuSerSerProGlyArgArgArgProArgGlyAspValGlnSerArg 1042
2635 GACAGCTTCG 2691
1043 AspAlaLeuAlaArgGlnLeuAsnArgLeuGlnLysThrArgLeuSerAlaAspMetAlaThr 1062
2692 GGACTGCACTGCTGCG 2751
1063 ValLeuGlnLeuLeuGln-ArgGlnMetThrLeu 1073
2752 TGCCCTGGCG 2811
1074 ---ValProAlaLysSerAla 1080
2812 CTGTGTGACACTGGGCGCATCTCTCTACTGCTGCGACCGCGCGCGCGCGCGCGCGCGCGCG 2871
1081 ---ValThrThrProGlyProGlyProThrSerThrSerProLeuLeuProValSerPr 1099
2872 AGTGGACACTGCG 2931
1099 oleu 1110
2932 GGTCCCGACGCTGCTC 2982
1111 -ValSerGlnPheMetAlaCysGlnGluLeuProProGly 1129
2983 ACCTCCACTGACACTGACAGCG 3042
1129 nGlnGlyProThrArgArgLeuSerLeuProGlyGlnLeuGlyAlaLeuThrSerGlnPr 1149
3043 CCTG 3046
1149 oleu 1150
Db 1149 oleu 1150
RESULT 11
US-09-735-995-2
Sequence 2, Application US/09735995
Patent No. US20010034024A1
GENERAL INFORMATION:
APPLICANT: Keating, Mark T.
APPLICANT: Splawski, Igor
TITLE OF INVENTION: MUTATIONS IN AND GENOMIC STRUCTURE OF HERG - A LONG QT
FILE REFERENCE: 2323-136
CURRENT APPLICATION NUMBER: US/09/735,995
CURRENT FILING DATE: 2000-12-14
PRIOR APPLICATION NUMBER: 09/226,012
PRIOR FILING DATE: 1999-01-06
NUMBER OF SEQ ID NOS: 116
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 1159
TYPE: PRT
ORGANISM: Homo sapiens
US-09-735-995-2
Alignment Scores:

Pred. No.: 1.83e-69 Length: 1159
 Score: 1551.00 Matches: 424
 Percent Similarity: 44.86% Conservative: 143
 Best Local Similarity: 33.54% Mismatches: 337
 Query Match: 25.47% Indels: 360
 DB: 10 Gaps: 38

US-09-965-830-1_COPY_6_3257 (1-3252) x US-09-735-995-2 (1-1159)

QY 1 ATGCCGGCCATCGGGCCCTCCCTGCGCTCAGAACACCTCTCTGAGACACATCGCTACG 60
 Db 1 MetProValArgArgGlyHisValAlaProGlnAsnThrPheLeuAspThrIleIleArg 20
 QY 61 CGCTTCACGGCAGCAGCAGACAGTCTGTCTGTGGGCAACGCCAGCGGGGCTCTTC 120
 Db 21 LysPheIleuGlnGlnSerArgLysPheIleIleAlaAsnIleArgValGluAsnGly 39
 QY 121 CGCTGTCTACTGCTGTGATGGCTTCTGTGACCTCAGGGCTCTCCGGGCTGAGCTC 180
 Db 40 AlaValIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 59
 QY 181 ATGCAGCGGGGCTGTGCT 240
 Db 60 MetGlnArgProCysThrCysAspPheLeuHisGlyProArgThrGlnIleArgAlaAla 79
 QY 241 CAACAGATCCGACAGCGCTCGAGCAGACAGAGAGTTCAGAGCTGATGCTGATC 300
 Db 80 AlaGlnIleAlaGlnAlaIleuLeuGlyAlaGlnIleuArgLysValGluIleAlaPheTyr 99
 QY 301 CGGAAGAGCGGGCTCCCGCTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 360
 Db 100 ArgLysAspGlySerCysPheLeuGlyLeuValAspValAlaProValLysAsnGluAsp 119
 QY 361 GGGAGAGTGGCT 399
 Db 120 GlyAlaValAlaIleMetPheIleLeuAsnPheGluValAlaMetGluLysAspMetValGly 139
 QY 400 -----AGCGAAACCAAGACCGAGGGGCGCCGACAGATGG----- 435
 Db 140 SerProAlaHisAspThrAsnHisArgGlyProProThrSerThrLeuAlaProGlyArg 159
 QY 435 ----- 435
 Db 160 AlaIleThrPheArgLeuLysLeuProAlaLeuLeuAlaLeuThrAlaArgGlySerSer 179
 QY 436 ---AAGAGACAGAGTGTGGCGCGCGCGATATGCGCGGCG---ACGATCCAAAGGCTTC 489
 Db 180 ValArgSerGlyGlyAlaGly-GlyAlaGlyAla-ProGlyAlaValAlaValAspValAla 199
 QY 490 AATGCCAACCGGCG----- 503
 Db 199 splLeuThrProAlaAlaProSerSerGluSerLeuAlaLeuAspGluValThrAlaMet 219
 QY 504 -----GCGAGCGCGGGCGCTGCTCTA----- 524
 Db 219 spAsnHisValAlaGlyLeuGlyProAlaGluIleuArgAlaValAlaGlyProGlyLys 239
 QY 525 ---CCACCTGTCCGGCAGCTGACAGAGCAAGCCCAAGGCGCAAG---CACAGCTCAAT--- 576
 Db 239 serProArgSerAlaProGlyGlnLeu-ProSerProArgAlaHisSerLeuAsnPro 258
 QY 576 ----- 576
 Db 259 AspAlaSerGlySerSerCysSerLeuAlaArgThrArgSerArgLysCysAlaSer 278
 QY 577 -----AAGGGGTGTTGGGGAG 594
 Db 279 ValArgArgAlaSerSerAlaAspAspIleGluAlaMetArgAlaGlyValLeuProPro 298
 QY 595 AATCCAAAC----- 603
 Db 299 ProProArgHisAlaSerThrGlyAlaMetHisProLeuArgSerGlyLeuLeuAsnSer 318

QY 603 ----- 603
 Db 319 ThrSerAspSerAspLeuValArgTyrArgThrIleSerLysIleProGlnIleThrLeu 338
 QY 603 ----- 603
 Db 339 AsnPheValAspLeuLysGlyAspProPheLeuAlaSerProThrSerAspArgGluIle 358
 QY 603 ----- 603
 Db 359 IleAlaProLysIleLysGluArgThrHisAsnValThrGluLysValThrGlnValLeu 378
 QY 604 -----TTGCTGAGTACAAAGTACGCCCATCGGAGATCGGCTTC 645
 Db 379 SerLeuGlyAlaAspValLeuProGluTyrLysLeuGlnAlaProArgIleHisArgThr 398
 QY 646 ATCTGTGTGACAGTGTGGGCACTGAGAGCCACCTGGATGGCTTCATCTGCTGCGCACA 705
 Db 399 ThrIleuHisTyrSerProPheLysAlaValTrpAspThrLeuIleLeuLeuVal 418
 QY 706 CTCTATGTGGCTGTACCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 756
 Db 419 IleTyrThrAlaValPheThrProTyrSerAlaAlaPheLeuLysGluThrGluGlu 438
 QY 757 GAGCCAGTGGC-----GCCGCGCGCGCCGAGGCTGTGACCTGGCC 801
 Db 439 GlyProProAlaThrGlnGlyGlyTyrAlaGlyGlnProLeuAlaValAlaAspLeuIle 458
 QY 802 GTGAGAGTCTCTTCATCTGATGATGCTGATGATGCTGATGATGCTGATGATGCTGATG 861
 Db 459 ValAspIleMetPheIleValAspIleLeuIleAsnPheArgThrIleTyrValAsnAla 478
 QY 862 TCGGCGCAGGTGTGTTCGCCCAAGTCCATTGCTCCATGCTGACAGTCCAGTCTGCTTC 921
 Db 479 AsnGluGluValAlaSerHisProGlyArgIleAlaValHisTyrPheLysGlyTyrPhe 498
 QY 922 CTGCTGATGTCATCGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 981
 Db 499 LeuIleAspMetValAlaAlaIleProPheAspLeuLeu----- 511
 QY 982 TACTTGGGGC-----CATCTGAGAGAGGTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCT 1023
 Db 512 IlePheLysSerGlySerGluGluLeuIleLysLeuLeuLysThrAlaArgLeuLeuArg 531
 QY 1024 CTGCTGCGCTGCTCCGCGCTGAGACCGGATCGAGTACGACGCGCTGCTGCTGCTGCTGCT 1083
 Db 532 LeuValAlaArgAlaAlaGlyLysLeuAspArgTyrSerGluTyrGlyAlaAlaValLeuPhe 551
 QY 1084 CTGCTCATGGCGCTGTTCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1143
 Db 552 LeuLeuMetCysThrPheAlaLeuIleAlaHisIlePheAlaCysIleTyrAlaIle 571
 QY 1144 GCGCAGCGGAGATCGAGAGCAGAGATCGAGTGGCTGAGATGCTGCTGCTGCTGCTGCTGCT 1203
 Db 572 GlyAsnMetGluGlnProHisMetAspSer-----ArgIleGlyTyrLeuHisAsn 588
 QY 1204 CTGGCGCGCGCGAGTACAGTCCCTACTACTGCTGCGCGGAGCGGAGCGGAGCGGAGCG 1263
 Db 589 LeuGlyAspIleIleGlyLysProTyr-----Asn 598
 QY 1264 AGCTCCGCGCAGTACACACTGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 1223
 Db 599 SerSerLys----- 601
 QY 1324 CTGCTGGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1383
 Db 602 ---LeuGlyGlyProSerIleLysAspLysTyrValThrAlaLeuTyrPheThrPheSer 620
 QY 1384 AGCTTACACAGCGGTGGCTTGGCAGAGTGTCCGCCAACAGCAGCAGCAGCAGCAGCAGCAG 1443
 Db 621 SerLeuThrSerValGlyPheGlyAsnValSerProAsnThrAsnSerGluLysIlePhe 640
 QY 1444 TCATCTGACCATGCTCATCGCGCGCTGATGACAGCGGTGTGTTGGGAACGTGACG 1503

```

Db 641 SerIleGlyValMetLeuIleGlySerLeuMetLeuAlaSerIlePheGlyAsnValSer 660
QY 1504 GCCATCATCCAGGAGCATATGAGCCCGGCTTCTGTACACAGACGCGGAGCT 1563
Db 661 AlaIleIleGlnArgLeuTyrSerGlyThrAlaArgTyrHisThrGlnMetLeuArgVal 680
QY 1564 CGGAGCTACATCCGATCCAGCCGATCCAGAGCCCTCAAGAGCCGATGCTGAGTAC 1633
Db 681 ArgGlnPheIleArgPheHisGlnIleProAsnProLeuArgGlnArgLeuGlnTyr 700
QY 1624 TTCCAGGCCACCTGGGGGGGACAAATGCGATGACACACCGAGCTGCTGACAGGCTC 1683
Db 701 PheGlnHisAlaTrpSerTyrThrAsnGlyIleAspMetAsnAlaValLeuYsGlyPhe 720
QY 1684 CCGAGAGCTGGGGGAGCATGCGCATGCACTGACCTGACAGAGAGGCTGACAG---CTG 1740
Db 721 ProGlnCysLeuGlnAlaAspIleCysLeuHisLeuAsnArgSerLeuMetGlnHisCys 740
QY 1741 CCACGTGTGAGGGGCGACCCGCGCTGCTGCGGCGACATGCTGTGCGCCCTGCGGCC 1800
Db 741 LysProPheArgGlyAlaThrIlyGlyCysLeuArgAlaLeuAlaMetIlySerPheIlyThr 760
QY 1801 GCCCTTGCACGCGCGGAGATACCTCATCCAGGCGATGCGCTGACAGGCGCTGTAC 1860
Db 761 ThrHisAlaProProGlyAspThrLeuValHisAlaGlyAspLeuLeuThrAlaLeuTyr 780
QY 1861 TTGTGCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1920
Db 781 PheIleSerArgIlySerIleGlnIleLeuArgGlyIlyAspValValAlaIleIleGlnGly 800
QY 1921 AAGGGGACCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1980
Db 801 LysAsnAspIlePheGlyGlyProLeuAsnLeuTyrAlaArgProGlyLysSerAsnGly 820
QY 1981 GACGTGAGGGGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2040
Db 821 AspAlaArgAlaLeuThrTyrCysAspLeuHisIlySerIleHisArgAspArgLeuGln 840
QY 2041 AGCCTGCGCTGATCCCGAGATTTGCCCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2100
Db 841 ValLeuAspMetTyrProGlnPheSerAspHisPheTrpSerLeu-----GlnIle 858
QY 2101 AGCTACAACTG-----GGTGTGGGGGAGCTGCTGACAGAGTGAC 2142
Db 859 ThrPheAsnLeuArgAspThrAsnMetIleProGlySerProGlySerThrGlnLeuGln 878
QY 2143 ACCGATCCCTCCGAGCGGAGCAATACCTTATGCTCAACCGCTGAGAGAGAGAGAGAT 2202
Db 879 GlyGlyPheSerArgGlnArgLysArgLysLeuSerPheArgArgArgThrAspLysAsp 898
QY 2203 GGGAGAGAGGGGCGGAGGCTGCCAGCCCGACCTGATGAGCCCTCCAGCCCTGCTG 2262
Db 899 ThrGlnGln----- 901
QY 2263 TCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2322
Db 902 ---ProGlyGlnValSerAla-----LeuGlyProGlyArgAlaGly 914
QY 2323 CCGCGGCGCTGCTGATGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2382
Db 915 AlaGlyPro-----SerSerArgIlyArgProGlyGlyProTrpGlyLysSerProser 932
QY 2383 GCTGGCCCTTGTCTCCCA-----CGGGCCCTAGAGGG 2418
Db 933 SerGlyProSerProGlnSerSerGlnAspGlnGlyProGlyArgSerSerSerPro 952
QY 2419 CTAGGCGCTG-----CCGCCCATGCCATGAGATGCGCCGATGTAGAGCC 2466
Db 953 LeuArgLeuValProPheSerSerProArgProGlyGlnProGlyGlnPro 972
QY 2467 AGGGAGAGATGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2514

```

```

Db 973 ---LeuMetGlnAspCysGlnLysSerSerAspThrCysAsnProLeuSerGlyAlaPhe 991
QY 2515 -----TCTCTTTC-----CGCGGGGCGGAGCT 2538
Db 992 SerGlyValSerAsnIlePheSerPheTrpGlyAspSerArgIlyArgGlnTyrGlnGln 1011
QY 2539 GCGCCGGATGTACAGACAGCGCCCTCCCTGACACAGAGAGAGAGAGAGAGAGAGAGAG 2595
Db 1012 LeuProArgCys-----ProAlaProThrProSerLeuAsnIlePro 1026
QY 2596 -----CCCATGGGCCAGCGAGGCGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2634
Db 1027 LeuSerSerProGlyArgArgProArgGlyAspValAluSerArg-----Leu 1042
QY 2635 GACAGCTTGGGAGGCGGTGACAGAGCTGTACAGAGAGAGT---CTGACATGCGGGAA 2691
Db 1043 AspAlaLeuGlnArgGlnLeuAsnArgLeuGlnThrArgLeuSerAlaAspMetAlaThr 1062
QY 2692 GGACTGATCATCTTGGCGAGAGCTGTGCACTTCTGCTGCGCGCCACAGAGAGAGGTCG 2751
Db 1063 ValLeuGlnLeuLeuGln-ArgGlnMetThrLeu----- 1073
QY 2752 TGCCCTGGGATGCGGAGAGAGGCGCGCCAGACAGACCTCGGCTTGTGAGGCT 2811
Db 1074 -----ValProAlaTyrSerAla-- 1080
QY 2812 CTGTGTGAGACTGGGGGATCTCTCTACTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 2871
Db 1081 ---ValThrThrProGlyProGlyProThrSerThrSerProLeuLeuProValSerPr 1099
QY 2872 AGTGAGCTTGGCCCACTCTGCTGCGGGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTG 2931
Db 1099 OLeu-----ProThrLeuThrLeuAspSerLeuSerLIn----- 1110
QY 2932 GGTCCCGGAGGCTCT-----AGAGCTCCCGCTGCGCTGAGAGAGAGAGAGAGAG 2982
Db 1111 -ValSerGlnPheMetAlaCysGlnGlnLeuProProGly---AlaProGlnLeuProGln 1139
QY 2983 ACCTTCACCTGAGACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3042
Db 1129 ngIleGlyProThrArgArgLeuSerLeuProGlyGlnLeuGlnAlaLeuThrSerGlnPr 1149
QY 3043 CCTG 3046
Db 1149 OLeu 1150

```

RESULT 12
 US-09-735-995-4
 : Sequence 4, Application US/09735995
 : Patent No. US20010034024A1
 : GENERAL INFORMATION:
 : APPLICANT: Keating, Mark T.
 : TITLE OF INVENTION: MUTATIONS IN AND GENOMIC STRUCTURE OF HERG - A LONG QT
 : TITLE OF INVENTION: SYNDROME GENE
 : FILE REFERENCE: 2323-136
 : CURRENT APPLICATION NUMBER: US/09/735,995
 : CURRENT FILING DATE: 2000-12-14
 : PRIOR APPLICATION NUMBER: 09/226,012
 : PRIOR FILING DATE: 1999-01-06
 : NUMBER OF SEQ ID NOS: 116
 : SOFTWARE: PatentIn Ver. 2.0
 : SEQ ID NO 4
 : LENGTH: 1159
 : TYPE: PRN
 : ORGANISM: Homo sapiens
 : US-09-735-995-4

Alignment Scores:
 Pred. No.: 1.83e-69 Length: 1159
 Score: 1551.00 Matches: 424
 Percent Similarity: 44.86 Conservative: 143
 Best Local Similarity: 33.548 Mismatches: 337


```

Db 661 AAlaIleIleGlnArgLeuTyrSerGlyThrAlaArgTyrHisThrGlnMetLeuArgVal 680
QY 1564 CGGCACTACATCCGCAATCCACACGATATCCCAAGCCCTCAAGAGGCAATGCTGAGAGAC 1623
Db 681 ArgGlnPheIleArgPheHisGlnIleProAsnProLeuArgGlnArgLeuGlnIleTyr 700
QY 1624 TTCACAGCCACCTGGGGGGTGAACAAGGGCATGCACACACACGAGCTGCTGACAGACCTTC 1683
Db 701 PheGlnHisAlaIlePheSerTyrThrAsnGlyIleAspMetAsnAlaValLeuGlnGlyPhe 720
QY 1684 CCGACAGAGCTGGCGGCGACATGCACATGCACATGCACAGAGAGTCTGACAG--CTG 1740
Db 721 ProGlnCysLeuGlnAlaAspIleCysLeuHisLeuAsnArgSerLeuGlnHisCys 740
QY 1741 CCAGTGTGGAGCGGCGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1800
Db 741 LysProPheArgGlyAlaThrLysLysLysLysLysLysLysLysLysLysLysLysLys 760
QY 1801 GCCTTCTGACGCGGCGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1860
Db 761 ThrHisAlaProProGlyLysPheThrLeuValHisAlaGlyAspLeuThrAlaLeuTyr 780
QY 1861 TTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1920
Db 781 PheIleSerArgGlySerIleGlnIleLeuArgGlyAspValValAlaIleLeuGly 800
QY 1921 AAGGCGGACCTGATGCGGTGAGTGCCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1980
Db 801 LysAsnAspIlePheGlyGlnProLeuAsnLeuTyrAlaArgProGlyLysSerAsnGly 820
QY 1981 GACGTGAAGGGGCTGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2040
Db 821 AspValArgAlaLeuThrTyrCysAspLeuHisLysIleHisArgAspLeuGln 840
QY 2041 AGCCTTGCCTGATACCCGAGTTTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2100
Db 841 ValLeuAspMetTyrProGlnPheSerAspHisPheTrpSerLeu-----GlnIle 858
QY 2101 AGCTACACCTG-----GCTGCTGCGGCGGCGGCTGCGAGGTGAG 2142
Db 859 ThrPheAsnLeuArgAspThrAsnMetIleProGlySerProGlySerThrGlnLeuGln 878
QY 2143 ACACAGCTCCCTGAGCGGCGGCAATACCCCTTATGCCAGCTGCTATCCCACTGCAACAGCA 2202
Db 879 GlyGlyPheSerArgGlnArgLysArgLysLeuSerPheArgArgArgThrAspLysAsp 898
QY 2203 GGGGAGAGGCGGCGGCGGCTGCCAGCCCGGCTGATGAGCCCTCCAGCCCGCTGCTG 2262
Db 899 ThrGlnGln----- 901
QY 2263 TCCCTGCTGACATCTCTCATCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2322
Db 902 ----ProGlyGlnValSerAla-----LeuGlyProGlyArgAlaGly 914
QY 2323 CCCCAGGCTCGTCTAGTGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2382
Db 915 AlaGlyPro-----SerSerArgGlyArgProGlyGlyProGlyGlyGlnSerProSer 932
QY 2383 GCTGCGCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2418
Db 933 SerGlyProSerSerProGlnSerSerGlnAspGlnGlyProGlyArgSerSerSerPro 952
QY 2419 CTAGAGGCTG-----CCCCCATGCCATGAGTATGATGATGATGATGATGATGATGATGATGATG 2466
Db 953 LeuArgLeuValProPheSerSerProArgProProGlyGlnProProGlyGlyGlnPro 972
QY 2467 AGGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2514
Db 973 ----LeuMetGlnAspCysGlnLysSerSerAspThrCysAsnProLeuSerGlyAlaPhe 991
QY 2515 ----TTCCTTTC-----CGCTGGCGGCAAGTCT 2538

```

```

Db 992 SerGlyValSerAsnIlePheSerPheTrpLysAspSerArgLysArgGlnTyrGlnGln 1011
QY 2539 GCGCCGCAATATACAGACAGCCCTCCCTGAGACAGAGGCGGCTGCTGCTGCTGCTGCTGCTG 2595
Db 1012 LeuProArgCys-----ProAlaProThrProSerLeuLeuAsnIlePro 1026
QY 2596 -----CCCATGCGCCAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2634
Db 1027 LeuSerSerProGlyArgArgProArgGlyAspValGlnSerArg-----Leu 1042
QY 2635 GACAGCTTTCGAGAGGCGGCTGACAGAGCTGTCAGACAGGTG--CTGACAGTCCGGGAA 2691
Db 1043 AspAlaLeuGlnArgGlnLeuAsnArgLeuGlnuThrArgLeuSerAlaAspMetAlaThr 1062
QY 2692 GGACTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2751
Db 1063 ValLeuGlnLeuLeuGln-ArgGlnMetThrLeu----- 1073
QY 2752 TGCCCTCGGCGATCGGAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 2811
Db 1074 -----ValProProAlaTyrSerAla-- 1080
QY 2812 CTGTGTGTGAGACATGGGCGCATCTCTTACTGCTGACAGCCCGGCTGCTGCTGCTGCTGCTG 2871
Db 1081 ----ValThrThrProGlyProGlyProThrSerThrSerProLeuLeuProValSerPr 1099
QY 2872 AGTGGGACTTGGCGCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2931
Db 1099 Gln-----ProThrLeuThrLeuAspSerLeuSerGln----- 1110
QY 2932 GGTCCCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2982
Db 1111 -ValSerGlnPheMetAlaCysGlnGlnLeuProProGly--AlaProGlnLeuProGln 1129
QY 2983 ACCTTCACCTCAGACATCAGAGAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3042
Db 1129 ngLuglyProThrArgArgLeuSerLeuProGlyGlnLeuGlyAlaLeuThrSerGlnPr 1149
QY 3043 CCGG 3046
Db 1149 Gln 1150

RESULT 13
US-09-119-855-10
; Sequence 10, Application US/09119855
; Patent No. US2002009197A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Roy A.J.
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
; FILE REFERENCE: mmi-055
; CURRENT APPLICATION NUMBER: US/09/119,855
; CURRENT FILING DATE: 1998-07-21
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 1159
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-119-855-10

Alignment Scores:
Pred. NO.: 1.83e-69 Length: 1159
Score: 1551.00 Matches: 424
Percent Similarity: 44.86 Conservative: 143
Best Local Similarity: 33.54 Mismatches: 337
Query Match: 25.47 Indels: 360
DB: Gaps: 38

US-09-965-830-1_COPY_6_3257 (1-3252) x US-09-119-855-10 (1-1159)
QY 1 ATGCCGGCCGCGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 60
Db 1 MetProValArgArgGlyHisValAlaProGlnAsnThrPheLeuAspThrIleLeuArg 20

```

QY 61 CGCTTCACGACGACAGTAACCTTCGTGGGCAACGCCGCGGCGCTCTC 120
 Db 21 LysPheGluGlnSerAlaGlySPheLeuLeuAlaAsnAlaArgValGluAsnCys--- 39
 QY 121 CCGGTGCTACTGCTGTGATGGCTTCTGTACCTCAGCGGCTTCTCCGCGGCTGAGTGC 180
 Db 40 AlaValIleTyrCysAsnAspGlyPheCysGluLeuGlyTyrSerAlaGluVal 59
 QY 181 ATGACGCGGCGCTGCTCTCTCTCTCTTATGGGCCAGACACAGCTGAGCTGCTCGC 240
 Db 60 MetGlnArgProCysThrCysAspPheLeuHISGlyProArgThrGlnArgAlaAla 79
 QY 241 CACAGATCCGCAAGGCCCTGAGACGACGACAGAGATTCAGGCTGAGCTGATCCCTGAC 300
 Db 80 AlaGlnIleAlaGlnAlaLeuLeuGlyAlaGluGlnArgValGluIleAlaPheTyr 99
 QY 301 CGGAGACGCGGCTCCCTGCTGCTGCTGATGTATACCATTAAGATGAGAA 360
 Db 100 ArgLysAspGlySerCysPheLeuCysLeuValAspValAlaProValLysAsnGluAsp 119
 QY 361 GGGGAGGTGGCTCTCTCTCTA-----GTCTCTCAAGACATC----- 399
 Db 120 GlyAlaValIleMetPheIleLeuAsnPheGluValValMetGluLysAspMetValGly 139
 QY 400 -----ACGGAACCAAGAACCGAGGGGCGCCGACAGATG----- 435
 Db 140 SerProAlaHISAspThrAsnHISArgGlyProProThrSerThrPheLeuAlaProGlyArg 159
 QY 435 ----- 435
 Db 160 AlaLysThrPheArgLeuLysLeuProAlaLeuLeuAlaLeuThrAlaArgLysSer 179
 QY 436 ---AAGGAGACAGTGGTGGTGGCGCGCATATGGCGCGGCG---ACGATCCAAAGCTTC 489
 Db 180 ValArgSerGlyGlyAlaGly-GlyAlaGlyAla-ProGlyAlaValAlaValAspValAla 199
 QY 490 AATGCCAACCGGCG----- 503
 Db 199 splLeuThrProAlaAlaProSerSerGluSerLeuAlaLeuAspGluValThrAlaMetAla 219
 QY 504 -----GCGGAGCGCGGCGGCTCTCTA----- 524
 Db 219 spAsnHISValAlaGlyLeuGlyProAlaGluGlnArgArgAlaLeuValGlyProGlyLys 239
 QY 525 ---CCACCTGTCCGGGCTGTCAGAACGACCCCAAGGCGAAG---CACAGCTCAT--- 576
 Db 239 erProArgSerAlaProGlyGlnLeu-ProSerProArgAlaHISerLeuAsnPro 258
 QY 576 ----- 576
 Db 259 AspAlaSerGlySerSerCysSerLeuAlaArgThrArgSerArgGluSerCysAlaSer 278
 QY 577 -----AAGGGGCTGTTGGGAG 594
 Db 279 ValArgArgAlaSerSerAlaAspArgIleGluAlaMetAlaGlyAlaValLeuProPro 298
 QY 595 AAACCAAC----- 603
 Db 299 ProProArgHISAlaSerThrGlyAlaMetHISProLeuArgSerGlyLeuLeuAsnSer 318
 QY 603 ----- 603
 Db 319 ThrSerAspSerAspLeuValArgTyrArgThrIleSerLysIleProGlnIleThrLeu 338
 QY 603 ----- 603
 Db 339 AsnPheValAspLeuLysGlyAspProPheLeuAlaSerProThrSerAspArgGluIle 358
 QY 603 ----- 603
 Db 359 IleAlaProLysIleLysGluArgThrHISAsnValThrGluLysValThrGlnValLeu 378

QY 604 -----TTGCTGATGACAAAGTACGCGCATCGGAAAGTCCGCCCTTC 645
 Db 379 SerLeuGlyAlaAspValLeuProGluTyrLysLeuGlnAlaProAlaIleHISArgThr 398
 QY 646 ATCTGTGACCTGTGGGGGACCTAGACCACTGGATGGCTTCATCTGCTGCGCCACA 705
 Db 399 ThrLeuHISLysTyrSerProPheLysAlaValIleAspArgIleLeuLeuVal 418
 QY 706 CTATATGGGTGTCACTGTGCTCCCTACAGCTGTGTGTG-----AGCACAGCAAGG 756
 Db 419 IleTyrThrAlaValPheThrProTyrSerAlaAlaPheLeuLeuLysGluThrGluGlu 438
 QY 757 GAGCCAGTGC-----GCCCGGGCGCCGCCACCTGTGACCTGCGC 801
 Db 439 GlyProProAlaThrGluCysGlyTyrAlaGlyGlnProLeuAlaValAspLeuIle 458
 QY 802 GTGGAGTCTCTTCATCTGATGATGTGCTGAATTCGCTACCATGCTGTCCAG 861
 Db 459 ValAspIleMetPheIleValAspIleLeuIleAsnPheArgThrThrTyrValAspAla 478
 QY 862 TCGGCGCAGGTGGTGTGGCCCAAGTCCATTTGCTCCACATGCTACACACCTGCTGC 921
 Db 479 AsnGluGluValValSerHISProGlyArgGluAlaValHISLysTyrPheLysGlyTyrPhe 498
 QY 922 CTGCTGATGTCATCGACGCGCTGCCCTTGACCTGCTACATGCTTCAAGTCAACGTG 981
 Db 499 LeuIleAspMetValAlaAlaIleProPheAspLeuLeu----- 511
 QY 982 TACTCGGGGCGC-----CATCTGTGAAGAGGTGGCCCTGCTGCGC 1023
 Db 512 IlePheGlySerLysSerGluGluLeuIleGlyLeuLeuLysThrAlaArgLeuLeuArg 531
 QY 1024 CTGCTGCGCTGCTTCCGCGGTGGACCGGCTATCGAGACAGCGCGCTGCTGAC 1083
 Db 532 LeuValArgValAlaArgLysLeuAspArgTyrSerGluTyrGlyAlaValAlaValPhe 551
 QY 1084 CTGCTGATGCGCTGTGCTGCGCTGCTGCGCACTGGGCTGCTGCTGCTGCTTTCAT 1143
 Db 552 LeuLeuMetCysThrPheAlaLeuIleAlaHISLysThrLeuAlaGlyLysIleTyrAlaIle 571
 QY 1144 GGCACGCGGAGATGACAGACGACGACGATCCGAGCTGCTGAGATTTGCTGCTGCTGAG 1203
 Db 572 GlyAsnMetGluGlnProHISMetAspSer-----ArgIleGlyThrPheHISAsn 588
 QY 1204 CTGGCGCGCGGCTGAGACTCCCTACTACCTGCTGCGCGGCGGACGACCTGAGGAAAC 1263
 Db 589 LeuGlyAspGlnIleGlyLysProTyr-----Asn 598
 QY 1264 AGCTCCGCGCAGATGACAACTGACAGCAGCAGCAGGAGGCAAGCGGAGCGGCTGAG 1323
 Db 599 SerSerGly----- 601
 QY 1324 CTGCTGGGCGCGCTGCTGCGGACGCGCTACATCACCTCCCTACTCTGACACTGAC 1383
 Db 602 ---LeuGlyGlyProSerIleLysAspLysTyrValIleAlaLeuTyrPheThrPheSer 620
 QY 1384 AGCTTCACACGCGTGGCTTGGCAGACGTGTCGCGCAACAGCAGCAGCAGAGAGATCTTC 1443
 Db 621 SerLeuThrSerValGlyPheGlyAsnValSerProAsnThrAsnSerGluLysIlePhe 640
 QY 1444 TCCATCTGCACCATGCTGATGGCGCCCTGATGACAGCGGTGGTGTGGGAACGTGAC 1503
 Db 641 SerIleCysValMetLeuIleGlySerLeuMetTyrAlaSerIlePheGlyAsnValSer 660
 QY 1504 GCCATCATCCAGCGCATGACCGCGCGCTTCTGTACACAGCGCGACCGGACCTG 1563
 Db 661 AlaIleIleGlnAlaArgLeuTyrSerGlyThrAlaArgTyrHISThrGlnMetLeuArgVal 680
 QY 1564 CGGCACTACATCCGATCCACGATCCCAAGCGCCCTCAGCAGCGGATGCTGAGTAC 1623
 Db 681 ArgGluPheIleArgPheHISGlnIleProAsnProLeuArgGlnArgLeuGluGluTyr 700
 QY 1624 TTCAGGCGCACCTGGCGGTGACAAATGGCATGACACACAGGAGCTGCTCAGAGCTTC 1683

[illegible]

```

RESULT 14
US-10-192-440-8
: Sequence 8, Application US/10192440
: Publication No. US20030082718A1
: GENERAL INFORMATION:
: APPLICANT: Curtis, Rory A. J.
: TITLE OF INVENTION: 52908, A HUMAN POTASSIUM CHANNEL, AND
: TITLE OF INVENTION: USES THEREOF
: FILE REFERENCE: MP12001-009P1RNM
: CURRENT APPLICATION NUMBER: US/10/192,440
: CURRENT FILING DATE: 2002-07-10
: PRIOR APPLICATION NUMBER: 60/341,953
: PRIOR FILING DATE: 2001-12-19
: PRIOR APPLICATION NUMBER: 60/304,243
: PRIOR FILING DATE: 2001-07-10
: NUMBER OF SEQ ID NOS: 15
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 8
: LENGTH: 994
: TYPE: prf
: ORGANISM: Homo sapiens
US-10-192-440-8

Alignment Scores:
Pred. No.: 2,06e-67 Length: 994
Score: 1509.50 Matches: 392
Percent Similarity: 49.04% Conservative: 167
Best Local Similarity: 34.39% Mismatches: 336
Query Match: 24.79% Indels: 245
DB: 9 Gaps: 36

US-09-965-830-1_COPY_6_3257 (1-3252) x US-10-192-440-8 (1-994)

QY 1 ATGCGCGCCATGCGGGGCGCTCTGCGCGCCTGACGACACCTTCTGTGACACCATGCGTACG 60
||||| ||||| :|||
|||MeerProValArgArgGlyHsValAlaProGlnAsnThrTyLeuAspPrnHleIleArg 20
:::|||||
|||
CGCTTGACGGCAGCGACGACAGTACTTCGTGCTGGCGCAAGCGCCAGGAGGGGCGCTCTTC 120
|||||:|||||

```


Thu May 8 08:49:39 2003

us-09-965-830-1_copy_6_3257.rapb

Db 201 AsnLeuProGluTyrLysValAlaAlaIleArgLysSerProPheIleLeuLeuHisCys 220
QY 661 GGGCACTGAGAGCCACCTGGGATGGCTTCATCCCTGCGCACACTATGTGGCTGTC 720
Db 221 GlyAlaLeuArgAlaThrTTPaspGlyPheIleLeuLeuAlaThrLeuTyrValAlaVal 240
QY 721 ACTGTGCCCTACAGCCGTGTGTGTGAGCACAGACGAGGCCAGTGGCGGCCGCCGCCG 780
Db 241 ThrValProTyrSerValCysValSerThrAlaArgGluProSerAlaAlaArgGlyPro 260
QY 781 CCCAGCGTGTGACCTGGCGGTGGAGGTCCCTTCATCCCTGACATTTGCTGAATTC 840
Db 261 ProSerValCysAspLeuAlaValGluValLeuPheIleLeuAspIleValLeuAspPhe 280
QY 841 CGTACC 846
Db 281 ArgThr 282

Search completed: May 7, 2003, 16:05:50
Job time : 190 secs

